SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

	5			(,	A) L	ENGTI	H: 1.	2// 1	oase	pai	rs								
				()	в) т	YPE:	nuc.	leic	acio	d									
				(C) S'	TRANI	DEDNI	ESS:	botl	n									
				()	D) T	OPOL	OGY:	line	ear										
	10		(ii) MO:	LECU:	LE T	YPE:	cDN	Ą										
			(ix) FE	ATUR:	E:													
				(2	A) N.	AME/I	KEY:	CDS											
	15			()	B) L	OCAT:	ION:	1	1275										
			(xi) SE	QUEN	CE DI	ESCR:	IPTI	: : NC	SEQ :	ID NO	0:1:				٠			
		ATG	GTC	GAA	ATG	CTG	CTG	TTG	ACA	AGA	ATT	CTC	TTG	GTG	GGC	TTC	ATC		4 8
		Met	Val	Glu	Met	Leu	Leu	Leu	Thr	Arg	Ile	Leu	Leu	Val	Gly	Phe	Ile		
· .	20	1				5					10					15			
•		TGC	GCT	CTT	TTA	GTC	TCC	TCT	GGG	CTG	ACT	TGT	GGA	CCA	GGC	AGG	ĠGC		96
		Cys	Ala	Leu	Leu	Val	Ser	Ser	Gly	Leu	Thr	Cys	Gly	Pro	Gly	Arg	Gly		
					20					25					30				
٠.	25																		
		ATT	GGA	AAA	AGG	AGG	CAC	CCC	AAA	AAG	CTG	ACC	CCG	TTA	GCC	TAT	AAG	•	144
		Ile	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys		
				35					40					45					
	30					AAT													192
		Gln		Ile	Pro	Asn	Val		Glu	Lys	Thr	Leu		Ala	Ser	Gly	Arg		
			50					55					60						
		TAT	GAA	GGG	AAG	ATC	ACA	AGA	AAC	TCC	GAG	AGA	TTT	AAA	GAA	CTA	ACC		240
	35	Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr _.		
		65					70					75					80		
		CCA	AAT	TAC	AAC	CCT	GAC	ATT	ATT	TTT	AAG	GAT	GAA	GAG	AAC	ACG	GGA		288
		Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly		

GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly GAC CGC GTG CTG GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC

		Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr	
						245					250					255		
		GTC	ATC	GAG	ACG	CGG	CAG	CCC	CGG	GCC	CGG	CTG	CTA	CTG	ACG	GCG	GCC	816
	5	Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Leu	Thr	Ala	Ala	
					260	_			_	265					270			
		CAC	CTG	CTC	TTT	GTG	GCC	CCC	CAG	CAC	AAC	CAG	TCG	GAG	GCC	ACA	GGG	864
						Val												
	10			275					280					285			*	
	10																	
		TCC	ACC	AGT	GGC	CAG	GCG	CTC	TTC	GCC	AGC	AAC	GTG	AAG	ССТ	GGC	CAA	912
=						Gln												
Ħ.		001	290		0-1			295					300	-3-		1		
Ū	15		2,00										500					
L. C. C. C. C. C. C. C. C. C.	13	ССТ	GTC	ТАТ	GTG	CTG	GGC	GAG	GGC	GGG	CAG	CAG	CTG	CTG	CCG	GCG	ТСТ	960
e. J						Leu												300
Ŭ.		305	vai	- y -	• 41	Lou	310	o _z u	011	017	0111	315	Lou	200			320	
=		303					310					313					020	
_	20	GTC	CAC	AGC	GTC	TCA	ጥጥር	CGG	GAG	GAG	GCG	тсс	GGA	GCC	TAC	GCC	CCA	1008
	20					Ser												1000
= <u>i</u>		vai	1113	501	vai	325	пси	my	Olu	Oru	330	OCI	Gry	1114	1 y 1.	335	110	
d D						J 2 J					330					333		
		CTC	ACC	GCC	CAG	GGC	ACC	ΔͲϹ	CTC	ΔͲC	ם מ כ	CGG	GTG	TTG	GCC	TCC	ፕርር	1056
	25					Gly												1000
	23	beu.	1111	nια	340	Gry	1111	116	пси	345	21311	1119	vai	пси	350	501	Cys	
					340					343					330			
		TID C	CCC	CTC	<u>አ</u> ሞር	GAG	CNC	CAC	א כייי	TCC	CCC	CAT	ሞርር	CCC	ምም ር	CCA	CCA	1104
						Glu												1104
	20	ıyı	АТА	355	тте	GIU	GIU	птр	360	rrb	Ald	птѕ	пр	365	FILE	на	FIO	
	30			333					360					363				
		mm.c	000	mmo	C C T	070	000	O.T.O.	C.T.C	666	666	C.T.C.	тсс	CCA	C D TI	ccc	ccc	1150
						CAG												1152
		Pne	_	Leu	Ата	Gln	стх		Leu	АТА	Ата	Leu		Pro	Asp	сту	Ата	
			370					375					380					
	35																	
						GCC												1200
			Pro	Thr	Ala	Ala		Thr	Thr	Thr	Gly		His	Trp	Tyr	Ser		
		385					390					395					400	
		CTC	CTC	TAC	CGC	ATC	GGC	AGC	TGG	GTG	CTG	GAT	GGT	GAC	GCG	CTG	CAT	1248
											2//1							

	Leu	Leu	Tyr	Arg	Ile 405	Gly	Ser	Trp	Val	Leu 410	Asp	Gly	Asp	Ala	Leu 415	His	
	CCG	CTG	GGC	ATG	GTG	GCA	CCG	GCC	AGC	TG							1277
5				Met													
				420					425								
10	(2)	INF	ORMA:	LION	FOR	SEQ	ID 1	10:2	:								
10		(i '	SEC	QUENC	CE C	HARA	TTER1	rstt(as:								
		(- /		A) LE						rs							
				3) T													
			((C) S1	rani	DEDNI	ESS:	bot	h								
15			([) T(OPOL	OGY:	line	ear									
		,				/DE	- DNI	n.*									
		(11)) MOI	LECUI	⊒E T	YPE:	CDN	4									
		(ix)) FEA	ATURE	Ξ:												
20				A) NA		KEY:	CDS										
			(F	3) LO	CAT:	ON:	1	1191									
		(xi)	SEC	QUENC	CE DI	ESCR:	IPTI(ON: S	SEQ :	ID NO	0:2:						
25	ATG	GCT	CTG	CCG	GCC	AGT	CTG	TTG	CCC	CTG	TGC	TGC	TTG	GCA	CTC	TTG	48
											Cys						
	1				5					10					15		
• •											CGA						96
30	Ala	Leu	Ser		Gln	Ser	Cys	Gly		Gly	Arg	Gly	Pro		Gly	Arg	
				20					25					30			
	CGG	CGT	TAT	GTG	CGC	AAG	CAA	CTT	GTG	CCT	CTG	СТА	TAC	AAG	CAG	TTT	144
	Arg	Arg	Tyr	Val	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe	
35			35					40					45				
											GCG						192
	Val		Ser	Met	Pro	Glu		Thr	Leu	Gly	Ala		Gly	Pro	Ala	Glu	
		50					55					60					

	GGG	AGG	GTA	ACA	AGG	GGG	TCG	GAG	CGC	TTC	CGG	GAC	CTC	GTA	CCC	AAC	240
				Thr													
	65	5			J	70			5		75					80	
5																	
	TAC	AAC	CCC	GAC	ATA	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGC	GGC	GCA	GAC	288
				Asp													
	_			_	85				_	90					95	_	
10	CGC	CTG	ATG	ACA	GAG	CGT	TGC	AAA	GAG	CGG	GTG	AAC	GCT	СТА	GCC	ATC	336
	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
				100					105					110			
	GCG	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTA	CGC	CTA	CGT	GTG	ACT	GAA	GGC	384
15	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
			115					120					125				
	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCA	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	432
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
20		130					135					140					
				GAC													480
		Ala	Leu	Asp	Ile		Thr	Ser	Asp	Arg		Arg	Asn	Lys	Tyr		
~ ~	145					150					155					160	
25			000	202	0.50	000	ama	<i>a</i>	000			~~~	maa	0.00			5.0.0
				CGC													528
	Leu	Leu	Ala	Arg		АІа	vaı	GIU	Ата	_	Pne	Asp	Trp	vai	-	Tyr	
					165					170					175		
30	GAG	ጥርር	CGC	AAC	CAC	ል ጥ C	CDC	СТД	ጥርር	GTC	מממ	CCT	СДТ	ממכ	ጥ ሮ አ	СТС	576
,,				Asn													370
	Giu	561	nrg	180	1113	110	1113	Vai	185	Val	БуЗ	ALG	пор	190	JCI	Бей	
				100					100					130			
	GCG	GTC	CGA	GCC	GGA	GGC	TGC	ттт	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTG	` 624
35				Ala													
			195		_	_	-	200		-			205		_		
	CGG	AGC	GGC	GAA	CGG	AAG	GGG	CTG	AGG	GAA	СТА	CAT	CGT	GGT	GAC	TGG	672
	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	

		210					215					220					
5				GCT Ala													720
				GAC Asp													768
10				CGG													816
15				Arg 260 GCT					265					270			864
13				Ala													
20				CGC Arg													912
25				CTC Leu													960
				GTG Val	Phe					Ala					Leu		1008
30	AAC	GAC	GTC	CTC	325 GCC	TCC	TGC	TAC	GCG	330 GTT	СТА	GAG	AGT	CAC	335 CAG	ТGG	1056
				Leu 340													
35				GCC Ala													1104
	CTG	CTC	CCT	GGG	GGT	GCA	GTC	CAG	CCG	ACT	GGC	ATG	CAT	TGG	TAC	TCT	1152

	Leu		Pro	Gly	Gly	Ala		Gln	Pro	Thr	Gly		His	Trp	Tyr	Ser	
		370					375					380					
	CGC	CTC	CTT	TAC	CGC	TTG	GCC	GAG	GAG	TTA	ATG	GGC	TG				1190
5	Arg	Leu	Leu	Tyr	Arg	Leu	Ala	Glu	Glu	Leu	Met	Gly					
	385					390					395						
	(2)	INF	ORMA:	rion	FOR	SEO	ID 1	NO:3	•								
10						_											
		(i)) SE(QUENC	CE CI	HARAC	CTER	ISTIC	CS:								
			(]	A) LI	ENGTI	H: 12	281 k	oase	pair	rs							
			•	·	YPE:												
1.5				C) S.					า								
15			(1) T() POP(JGY:	T1116	ear									
		(ii)) MOI	LECUI	LE TY	YPE:	cDNA	E									
20		(ix)		ATURI		ZTI SZ	ana	`		•							•
				A) NA B) L(1233									
			1,1	J) 110	50111	. 011.		1233									
		(xi)) SE(QUENC	CE DE	ESCRI	PTIC	ON: S	SEQ I	ID NO	0:3:						
25																	
														CTG			48
		Ser	Pro	Ala	_	Leu	Arg	Pro	Arg		Arg	Phe	Cys	Leu		Leu	
	1				5					10					15		
30	CTG	CTG	CTG	CTT	CTG	GTG	CCG	GCG	GCG	CGG	GGC	TGC	GGG	CCG	GGC	CGG	96
	Leu	Leu	Leu	Leu	Leu	Val	Pro	Ala	Ala	Arg	Gly	Cys	Gly	Pro	Gly	Arg	
				20					25					30			
	CMC	CTC	ccc	N.C.C.	CCC	CCC	n.c.c	CCC	CCT	CCC	71 71 C	CTC	CTC	CCT	CTT	CCC	1 4 4
35														Pro			144
33	Val	vai	35	Del	my	my	1119	40	110	1129	Буб	БСС	45	110	Deu	nii	
	TAC	AAG	CAG	TTC	AGC	CCC	AAC	GTG	CCG	GAG	AAG	ACC	CTG	GGC	GCC	AGC	192
	Tyr	Lys	Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser	

7/61

		50					55					60					
	GGG	CGC	TAC	GAA	GGC	AAG	ATC	GCG	CGC	AGC	тст	GAG	CGC	TTC	AAA	GAG	240
	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	
5	65					70					75					80	
	CTC	ACC	CCC	AAC	TAC	AAT	CCC	GAC	ATC	ATC	TTC	AAG	GAC	GAG	GAG	AAC	288
	Leu	Thr	Pro	Asn	Tyr 85	Asn	Pro	Asp	Ile	Ile 90	Phe	Lys	Asp	Glu	Glu 95	Asn	
10					•												
	ACG	GGT	GCC	GAC	CGC	CTC	ATG	ACC	CAG	CGC	TGC	AAG	GAC	CGT	CTG	AAC	336
	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	
				100					105					110			
15	TCA	CTG	GCC	ATC	TCT	GTC	ATG	AAC	CAG	TGG	CCT	GGT	GTG	AAA	CTG	CGG	384
	Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	
			115					120					125				
	GTG	ACC	GAA	GGC	CGG	GAT	GAA	GAT	GGC	CAT	CAC	TCA	G.AG	GAG	TCT	TTA	432
20	Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	
		130					135					140					
	CAC	TAT	GAG	GGC	CGC	GCG	GTG	GAT	ATC	ACC	ACC	TCA	GAC	CGT	GAC	CGA	480
	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	-
25	145					150					155					160	
	AAT	AAG	TAT	GGA	CTG	CTG	GCG	CGC	TTA	GCA	GTG	GAG	GCC	GGC	TTC	GAC	528
	Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	
					165					170					175		
30																	
									CAC								576
	Trp	Val	Tyr	_	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser		Lys	Ser	
				180					185					190			
35	GAG	CAT	TCG	GCC	GCT	GCC	AAG	ACA	GGT	GGC	TGC	TTT	CCT	GCC	GGA	GCC	624
	Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
			195					200					205				
	CAG	GTG	CGC	CTA	GAG	AAC	GGG	GAG	CGT	GTG	GCC	CTG	TCA	GCT	GTA	AAG	672

	Gln	Val 210	Arg	Leu	Glu	Asn	Gly 215	Glu	Arg	Val	Ala	Leu 220	Ser	Ala	Val	Lys	
	CCA	GGA	GAC	.CGG	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	ACC	CCC	ACC	TTC	720
5	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
	225					230					235					240	
	AGT	GAT	GTG	CTT	ATT	TTC	CTG	GAC	CGC	GAG	CCA	AAC	CGG	CTG	AGA	GCT	768
	Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	
10					245					250					255		
•	TTC	CAG	GTC	ATC	GAG	ACT	CAG	GAT	CCT	CCG	CGT	CGG	CTG	GCG	CTC	ACG	816
	Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
				260					265					270			
15					~~~				~~~		~~ ~			~~~		~~~	0.54
								GCG									864
	Pro	Ата	275	Leu	Leu	Pne	ire	Ala 280	Asp	ASII	птз	1111	285	PIO	Ald	Ala	
			275					200					203				
20	CAC	TTC	CGG	GCC	ACA	TTT	GCC	AGC	CAT	GTG	CAA	CCA	GGC	CAA	TAT	GTG	912
	His	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	
		290					295					300					
	CTG	GTA	TCA	GGG	GTA	CCA	GGC	CTC	CAG	CCT	GCT	CGG	GTG	GCA	GCT	GTC	960
25		Val	Ser	Gly	Val	Pro	Gly	Leu	Gln	Pro		Arg	Val	Ala	Ala		
	305					310					315					320	
	ጥርር	ACC.	C Λ C	CTC	GCC	CTT	GGG	TCC	ייי ע ייי	CCT	ССТ	CTC	$\Delta \subset \Delta$	ACC	$C\Delta T$	GGG	1008
								Ser									1000
30					325	200	017	202	- 7 -	330		200		9	335	4 - 1	
	ACA	CTT	GTG	GTG	GAG	GAT	GTG	GTG	GCC	TCC	TGC	TTT	GCA	GCT	GTG	GCT	1056
	Thr	Leu	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	
				340					345					350			
35																	
	GAC	CAC	CAT	CTG	GCT	CAG	TTG	GCC	TTC	TGG	CCC	CTG	CGA	CTG	TTT	CCC	1104
	Asp	His		Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu		Leu	Phe	Pro	
			355					360					365				

	AGT TTG GCA TGG GGC AGC TGG ACC CCA AGT GAG GGT GTT CAC TCC TAC	1152
	Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr	
	370 375 380	
5	CCT CAG ATG CTC TAC CGC CTG GGG CGT CTC TTG CTA GAA GAG AGC ACC	1200
	Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr	
	385 390 395 400	
	TTC CAT CCA CTG GGC ATG TCT GGG GCA GGA AGC TGAAGGGACT CTAACCACTG	1253
10	Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser	1233
10	405 410	
	CCCTCCTGGA ACTGCTGTGC GTGGATCC	1281
15		
	(2) INFORMATION FOR SEQ ID NO:4:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 1313 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: both (D) TOPOLOGY: linear	
	(b) TOPOLOGI. IIMeal	
	(ii) MOLECULE TYPE: cDNA	
25		
	(ix) FEATURE:	
	(A) NAME/KEY: CDS	
	(B) LOCATION: 11314	
30		,
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
	ATG CTG CTG CTG GCC AGA TGT TTT CTG GTG ATC CTT GCT TCC TCG	10
35	Met Leu Leu Leu Àla Arq Cys Phe Leu Val Ile Leu Ala Ser Ser	48
55	1 5 10 Leu Leu Leu Ara Arg Cys Phe Leu Val IIe Leu Ara Ser Ser	
	CTG CTG GTG TGC CCC GGG CTG GCC TGT GGG CCC GGC AGG GGG TTT GGA	96
	Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly	

				20					25					30			
												GCC					144
_	Lys	Arg	_	His	Pro	Lys	Lys		Thr	Pro	Leu	Ala	-	Lys	Gln	Phe	
5			35					40					45				
	ATT	CCC	AAC	GTA	GCC	GAG	AAG	ACC	СТА	GGG	GCC.	AGC	GGC	AGA	TAT	GAA	192
												Ser					
		50					- 55					60	_				
10																	
	GGG	AAG	ATC	ACA	AGA	AAC	TCC	GAA	CGA	TTT	AAG	GAA	CTC	ACC	CCC	AAT	240
	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	
	65					70					75					80	
1.5	m 7 C	770	000	C7 C	7 m.c	יי מיי	mmm	7.7.0	C T M	CT C	C 7 7	7.7.0	7.00	CCA	CCA	C D C	200
15												AAC					288
	Tyr	ASII	Pro	Asp	85	тте	rne	гуѕ	Asp	90	Glu	Asn	TIIL	GIY	95	ASP	
					0.5					90					93		
	CGG	CTG	ATG	ACT	CAG	.AGG	TGC	AAA	GAC	AAG	TTA	AAT	GCC	TTG	GCC	ATC	336
20	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	
				100					105					110			
	TCT	GTG	ATG	AAC	CAG	TGG	CCT	GGA	GTG	AGG	CTG	CGA	GTG	ACC	GAG	GGC	384
	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
25			115					120					125				
		G 3 . T	a. a		222	O.T. M	C 7	T C T	07.0	07.0	m.c.m	G.E.R	07.0	m n m	G T G	000	420
												CTA					432
	Trp		GIU	Asp	GTÀ	HIS		ser	Glu	GIU	ser	Leu	HIS	Tyr	Giu	сту	
30		130					135					140					
30	CGA	GCA	GTG	GAC	ΔTC	ACC	ACG	ፐርር	GAC	CGG	GAC	CGC	AGC	AAG	ТΑС	GGC	480
												Arg					100
	145	1114	, 42	пор		150		502		9	155	9	001	210	+ 1 -	160	
					•												
35	ATG	CTG	GCT	CGC	CTG	GCT	GTG	GAA	GCA	GGT	TTC	GAC	TGG	GTC	TAC	TAT	528
	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
					165					170					175		
	GAA	TCC	AAA	GCT	CAC	ATC	CAC	TGT	TCT	GTG	AAA	GCA	GAG	AAC	TCC	GTG	576

	Glu	Ser	Lys	Ala 180	His	Ile	His	Cys	Ser 185	Val	Lys	Ala	Glu	Asn 190	Ser	Val		
	GCG	GCC	AAA	TCC	GGC	GGC	TGT	TTC	CCG	GGA	TCC	GCC	ACC	GTG	CAC	CTG	6	524
5	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu		
			195					200					205					
	GAG	CAG	GGC	GGC	ACC	AAG	CTG	GTG	AAG	GAC	TTA	CGT	CCC	GGA	GAC	CGC	6	572
	Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg		
10		210					215					220						
	GTG	CT.G	GCG	GCT	GAC	GAC	CAG	GGC	CGG	CTG	CTG	TAC	AGC	GAC	TTC	CTC	7	720
	Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu		
	225					230					235					240		
15																		
						GAC											7	768
	Tnr	Pne	Leu	Asp	Arg 245	Asp	GIU	GIŸ	ATS	Lys 250	rys	vaı	Pne	Tyr	255	ile		
			ż		243					200					233			
20	GAG	ACG	CTG	GAG	CCG	CGC	GAG	CGC	CTG	CTG	CTC	ACC	GCC	GCG	CAC	CTG	8	316
	Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu		
				260					265					270				
	CTC	TTC	GTG	GCG	CCG	CAC	AAC	GAC	TCG	GGG	CCC	ACG	CCC	GGG-	CCA	AGC	8	364
25	Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser		
			275					280					285					
	GCG	CTC	TTT	GCC	AGC	CGC	GTG	CGC	CCC	GGG	CAG	CGC	GTG	TAC	GTG	GTG	9	912
	Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val		
30		290					295					300						
						GAC											9	60
		Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu		Ala	Ala	Val	His			
35	305					310					315					320		
55	GTG	ACG	CTG	CGA	GAG	GAG	GAG	GCG	GGC	GCG	TAC	GCG	CCG	СТС	ACG	GCG	10	008
						Glu											10	
				,	325				-	330	-				335			

	CAC	GGC	ACC	ATT	CTC	ATC	AAC	CGG	GTG	CTC	GCC	TCG	TGC	TAC	GCT	GTC	1056
	His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	
				340					345					350			
5	ATC	GAG	GAG	CAC	AGC	TGG	GCA	CAC	CGG	GCC	TTC	GCG	CCT	TTC	CGC	CTG	1104
	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Arq	Ala	Phe	Ala	Pro	Phe	Arq	Leu	
			355					360	,				365				
	GCG	CAC	GCG	CTG	CTG	GCC	GCG	CTG	GCA	CCC	GCC	CGC	ACG	GAC	GGC	GGG	1152
10	Ala	His	Ala	Leu	Ŀeu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Gly	Gly	
		370					375					380					
	GGC	GGG	GGC	AGC	ATC	CCT	GCA	GCG	CAA	TCT	GCA	ACG	GAA	GCG	AGG	GGC	1200
	Gly	Gly	Glу	Ser	Ile	Pro	Ala	Ala	Gln	Ser	Ala	Thr	Glu	Ala	Arg	Gly	•
15	385					390					395					400	
	GCG	GAG	CCG	ACT	GCG	GGC	ATC	CAC	TGG.	TAC	TCG	CAG	CTG	CTC	TAC	CAC	1248
	Ala	Glu	Pro	Thr	Ala	Gly	Ile	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	His	
					405					410					415		
20																	
	ATT	GGC	ACC	T'GG	CTG	TTG	GAC	AGC	GAG	ACC	ATG	.CAT	CCC.	TTG	GGA	ATG	1296
	Ile	Gly	Thr	Trp	Leu	Leu	Asp	Ser	Glu	Thr	Met	His	Pro	Leu	Gly	Met	
				420					425					430			
25	GCG	GTC	AAG	TCC	AGC	TG											1313
	Ala	Val	Lys	Ser	Ser												
			435														

30 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

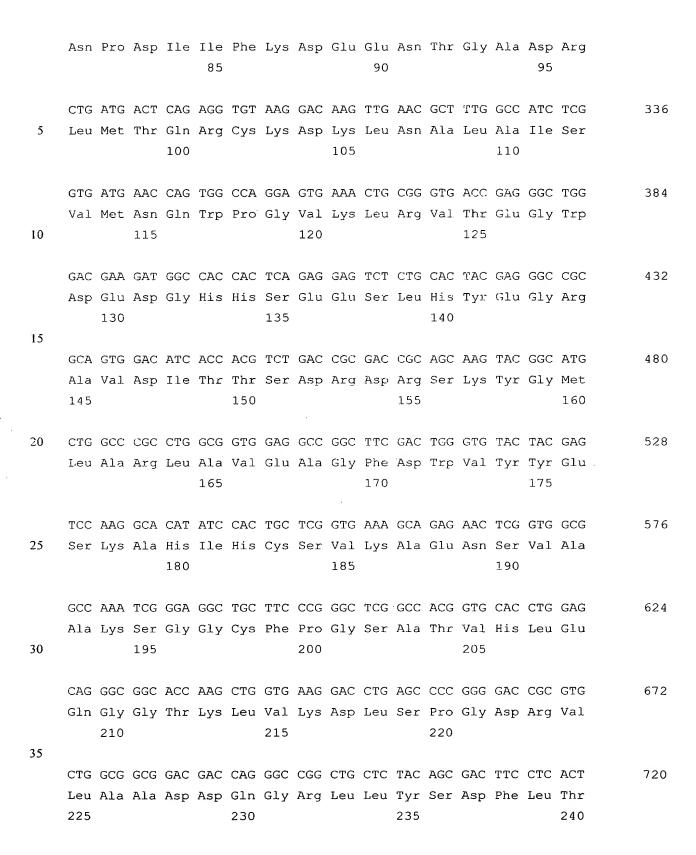
					OCAT:			1257									
5																	
		(xi)) SEC	QUENC	CE DE	ESCR	IPTIC	ЭN: 3	SEQ I	ID NO	D:5:						
	ATG	CGG	CTT	TTG	ACG	AGA	GTG	CTG	CTG	GTG	TCT	CTT	CTC	ACT	CTG	TCC	48
10	Met	Arg	Leu	Leu	Thr	Arg	Val	Leu	Leu	Val	Ser	Lėu	Leu	Thr	Leu	Ser	
	1				5					10					15		
	TTG	GTG	GTG	TCC	GGA	CTG	GCC	TGC	GGT	CCT	GGC	AGA	GGC	TAC	GGC	AGA	96
	Leu	Val	Val	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Tyr	Gly	Arg	
15				20					25					30			
	AGA	AGA	CAT	CCG	AAG	AAG	CTG	ACA	CCT	CTC	GCC	TAC	AAG	CAG	TTC	ATA	144
	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	
			35					40					45				
20																	
	CCT	AAT	GTC	GCG	GAG	AAG	ACC	TTA	GGG	GCC	AGC	GGC	AGA	TAC	GÄG	GGC	192
	Pro		Val	Ala	Glu	Lys		Leu	Gly	Ala	Ser		Arg	Tyr	Glu	G17.	
		50					55					60					
25	AAG	ATA	ACG	CGC	AAT	TCG	GAG	AGA	TTT	AAA	GAA	CTT	ACT	CCA	AAT	TAC	240
	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
	65					70					75					80	
	AAT	CCC	GAC	ATT	ATC	ттт	AAG	GAT	GAG	GAG	AAC	ACG	GGA	GCG	GAC	AGG	288
30	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	
					85					90					95		
	CTC	ATG	ACA	CAG	AGA	TGC	AAA	GAC	AAG	CTG	AAC	TCG	CTG	GCC	ATC	TCT	336
	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser	
35				100					105					110			
	GTA	ATG	AAC	CAC	TGG	CCA	GGG	GTT	AAG	CTG	CGT	GTG	ACA	GAG	GGC	TGG	384
	Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	
			115					120					125				

	GAT	GAG	GAC	GGT	CAC	CAT	TTT	GAA	GAA	TCA	CTC	CAC	TAC	GAG	GGA	AGA	432
	Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	
		130					135					140					
5																	
	GCT	GTT	GAT	ATT	ACC	ACC	TCT	GAC	CGA	GAC	AAG	AGC	AAA	TAC	GGG	ACA	480
	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr	
	145					150					155					160	
10	CTG	TCT	CGC	CTA	GCT	GTG	GAG	GCT	GGA	TTT	GAC	TGG	GTC	TAT	TAC	GAG	528
	Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	
					165					170					175		
	TCC	AAA	GCC	CAC	ATT	CAT	TGC	TCT	GTC	AAA	GCA	GAA	AAT	TCG	GTT	GCT	576
15	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	
				180					185					190			
-																	
	GCG	AAA	TCT	GGG	GGC	TGT	TTC	CCA	GGT	TCG	GCT	CTG	GTC	TCG	CTC	CAG	624
	Ala	Lÿs	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Leu	Val	Ser	Leu	Gln	
20			195					200					205				
																	-
•	GAC	GGA	GGA	CAG	AAG	GCC	GTG	AAG	GAC	CTG	AAC	CCC	GGA	GAC	AAG	GTG	672
	Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val	
		210					215					220					
25																	
	CTG	GCG	GCA	GAC	AGC	GCG	GGA	AAC	CTG	GTG	TTC	AGC	GAC	TTC	ATC	ATG	720
	Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met	
	225					230					235					240	
30	TTC	ACA	GAC	CGA	GAC	TCC	ACG	ACG	CGA	CGT	GTG	TTT	TAC	GTC	ATA	GAA	768
	Phe	Thr	Asp	Arg	Asp	Ser	Thr	Thr	Arg	Arg	Val	Phe	Tyr	Val	Ile	Glu	
					245					250					255		
	ACG	CAA	GAA	CCC	GTT	GAA	AAG	ATC	ACC	CTC	ACC	GCC	GCT	CAC	CTC	CTT	816
35	Thr	Gln	Glu	Pro	Val	Glu	Lys	Ile	Thr	Leu	Thr	Ala	Ala	His	Leu	Leu	
				260					265					270			
	TTT	GTC	CTC	GAC	AAC	TCA	ACG	GAA	GAT	CTC	CAC	ACC	ATG	ACC	GCC	GCG	864
	Phe	Val	Leu	Asp	Asn	Ser	Thr	Glu	Asp	Leu	His	Thr	Met	Thr	Ala	Ala	
								•									

			275					280					285					
												ATG					91	.2
5	Tyr	A1a 290	Ser	Ser	Val	Arg	A1a 295	Gly	Gln	Lys	Val	Met 300	Val	Val	Asp	Asp		
												ATA Ile					96	60
10															9			
												GGG Gly					100	8 (8
	44.2																	
15												GAG Glu					105	06
	ccc	СЪТ	ጥጥር		ምም ር	ece	ccc	GCC		ርሞር	ጥልጥ	TAT	ጥ ልር		тса	TCΔ	110	1.4
20												Tyr						, 1
	TTC	CTG	TCC	CCC	AAA	ACT	CCA	GCA	GTC	GGT	CCA	ATG	CGA	CTT	TAC	AAC	115	2
25	Phe	Leu 370	Ser	Pro	Lys	Thr	Pro 375	Ala	Val	Gly	Pro	Met 380	Arg	Leu	Tyr	Asn		
												CAT His					120	0
30	385	,	-			390			4		395				-	400		
												GGG Gly					124	8
					405					410					415			
35	TCA Ser	AGC Ser	TG														125	6

(2) INFORMATION FOR SEQ ID NO:6:

		(1		 Jorno													
_								base	-	rs							
5			(1	•				aci									
			((sin	gle								
			(1	D) T(OPOL	OGY:	lin	ear									
10		(ii) MO:	LECUI	LE T	YPE:	cDN	Α.									
		(ix) FE	ATURI	Ξ:												
				A) N													
1.5			(]	B) L(OCAT:	ION:	1	1425									
15																	
		(xi) SE	OUENC	CE DI	ESCR	IPTI	ON:	SEO :	ID N	0:6:						
		,	,														
	ATG	CTG	CTG	CTG	GCG	AGA	TGT	CTG	CTG	CTA	GTC	СТС	GTC	TCC	TCG	CTG	48
20	Met	Leu	Leu	Leu	Ala	Arg	Cys	Leu	Leu	Leu	Val	Leu	Val	Ser	Ser	Leu	
	1				5					10					15		
	СПС	C III A	mcc.	тос	CCA	CMC	666	mca.	CCA	000	ccc	7 C C	ccc	mm/c	ccc	7 7 C	0.0
•														TTC Phe			96
25	ьeu	vaı	Cys	20	GIY	ьеи	ALG	Суз	25	FIO	GIŸ	Arg	GIŸ	30	Gry	цуз	÷ *
	AGG	AGG	CAC	CCC	AAA	AAG	CTG	ACC	ССТ	TTA	GCC	TAC	AAG	CAG	TTT	ATC	144
	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	
			35					40					45				
30																	
														TAT			192
	Pro		Val	Ala	Glu	Lys		Leu	Gly	Ala	Ser	_	Arg	Tyr	Glu	Gly	
		50					55					60					
35	AAG	ATC	TCC	AGA	AAC	TCC	GAG	CGA	TTT	AAG	GAA	CTC	ACC	CCC	AAT	TAC	240
	Lys	Ile	Ser	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
	65					70					75					80	
	AAC	CCC	GAC	ATC	ATA	TTT	AAG	GAT				ACC	GGA	GCG	GAC	AGG	288
										17/61							



	TTC	CTG	GAC	CGC	GAC	GAC	GGC	GCC	AAG	AAG	GTC	TTC	TAC	GTG	ATC	GAG	768
	Phe	Leu	Asp	Arg	_	Asp	Gly	Ala	Lys	_	Val	Phe	Tyr	Val		Glu	
					245					250					255		
5	ACG	CGG	GAG	CCG	CGC	GAG	CGC	CTG	CTG	CTC	ACC	GCC	GCG	CAC	CTG	CTC	816
	Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu	
				260					265					270			
	u u u	CTC	CCC	CCC	CAC	7 A C	CAC	TCG	CCC	NCC.	ccc	CAC	ccc	CAC	CCG	TCC	864
10								Ser									F00
			275				1	280			1		285				
								GGG									912
1.5	Ser		Ser	Gly	Pro	Pro		Gly	Gly	Ala	Leu		Pro	Arg	Ala	Leu	
15		290					295					300					
	TTC	GCC	AGC	CGC	GTG	CGC	CCG	GGC	CAG	CGC	GTG	TAC	GTG	GTG	GCC	GAG	960
	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	Ala	Glu	
	305					310					315					320	
20												*					
								CTG									1008
	Arg	Asp	GLy	Asp	Arg 325	Arg	Leu	Leu	Pro	330	Ala	vaı	His	ser	335	Thr	
					323					550					333		
25	СТА	AGC	GAG	GAG	GCC	GCG	GGC	GCC	TAC	GCG	CCG	CTC.	ACG	GCC	CAG	GGC	1056
	Leu	Ser	Glu	Glu	Ala	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	Gln	Gly	
				340					345					350			
	N.C.C	አ ጥጥ	CTC	አ ሞ C	አአር	CCC	CTC	CTG	CCC	TCG	ጥርር	ጥእር	GCC	CTC	አጥር	GNG	· 1104
30								Leu									1104
			355			,		360			-	_	365				•
	GAG	CAC	AGC	TGG	GCG	CAC	CGG	GCC	TTC	GCG	CCC	TTC	CGC	CTG	GCG	CAC	1152
	Glu		Ser	Trp	Ala	His	-	Ala	Phe	Ala	Pro		Arg	Leu	Ala	His	
35		370					375					380					
	GCG	СТС	СТС	GCT	GCA	CTG	GCG	CCC	GCG	CGC	ACG	GAC	CGC	GGC	GGG	GAC	1200
								Pro									
	385					390					395					400	

	AGC	GGC	GGC	GGG	GAC	CGC	GGG	GGC	GGC	GGC	GGC	AGA	GTA	GCC	CTA	ACC	1248
	Ser	Gly	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr	
					405					410					415		
5																	
	GCT	CCA	GGT	GCT	GCC	GAC	GCT	CCG	GGT	GCG	GGG	GCC	ACC	GCG	GGC	ATC	1296
	Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile	
				420					425					430			
10	CAC	TGG	TAC	TCG	CAG	CTG	CTC	TAC	CAA	ATA	GGC	ACC	TGG	CTC	CTG	GAC	1344
	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	Gln	Ile	Gly	Thr	Trp	Leu	Leu	Asp	
			435					440					445				
	AGC	GAG	GCC	CTG	CAC	CCG	CTG	GGC	ATG	GCG	GTC	AAG	TCC	AGC	NNN	AGC	1392
15	Ser	Glu	Ala	Leu	His	Pro	Leu	Gly	Met	Ala	Val	Lys	Ser	Ser	Xaa	Ser	
		450					455					460					
	CGG	GGG	GCC	GGG	GGA	GGG	GCG	CGG	GAG	GGG	GCC						1425
	Arg	Gly	Ala	GTA	Gly	Gly	Ala	Arg	Glu	Gly	Ala						
20	465					470					475						

(2) INFORMATION FOR SEQ ID NO:7:

25

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
- 35 (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 51..1283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	CATO	CAGC	CCA (CCAG	GAGA(CC TO	CGCC	CGCC	G CT	CCCC	CGGG	CTC	CCCG	GCC I	ATG '	гст	56
														ľ	Met :	Ser	
5															1		
	CCC	GCC	CGG	CTC	CGG	CCC	CGA	CTG	CAC	TTC	TGC	CTG	GTC	CTG	TTG	CTG	104
	Pro	Ala	Arg	Leu	Arg	Pro	Arg	Leu	His	Phe	Cys	Leu	Val	Leu	Leu	Leu	
			5					10					15				
10																	
	CTG	CTG	GTG	GTG	CCC	GCG	GCA	TGG	GGC	TGC	GGG	CCG	GGT	CGG	GTG	GTG	152
	Leu	Leu	Val	Val	Pro	Ala	Ala	Trp	Gly	Cys	Gly	Pro	Gly	Arg	Val	Val	
		20					25					30					
15	GGC	AGC	CGC	CGG	CGA	CCG	CCA	CGC	AAA	CTC	GTG	CCG	CTC	GCC	TAC	AAG	200
	Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala	l'yr	Lys	
	35					40					45					50	
	CAG	TTC	AGC	CCC	AAT	GTG	CCC	GAG	AAG	ACC	CTG	GGC	GCC	AGC	GGA	CGC	248
20	Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	
					55					60					65		
	TAT	GAA	GGC	AAG	ATC	GCT	CGC	AGC	TCC	GAG	CGC	TTC	AAG	GAG	CTC	ACC	296
	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	
25				70					75					80			
	CCC	AAT	TAC	AAT	CCA	GAC	ATC	ATC	TTC	AAG	GAC	GAG	GAG	AAC	ACA	GGC	344
	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	
			85					90					95				
30																	
	GCC	GAC	CGC	CTC	ATG	ACC	CAG	CGC	TGC	AAG	GAC	CGC	CTG	AAC	TCG	CTG	392
	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	Ser	Leu	
		100					105					110					
35	GCT	ATC	TCG	GTG	ATG	AAC	CAG	TGG	CCC	GGT	GTG	AAG	CTG	CGG	GTG	ACC	440
	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
	115					120		_		_	125			_		130	
	GAG	GGC	TGG	GAC	GAG	GAC	GGC	CAC	CAC	TCA	GAG	GAG	TCC	CTG	CAT	TAT	488
										21/61							

	Glu	Gly	Trp	Asp	Glu 135	Asp	Gly	His	His	Ser 140	Glu	Glu	Ser	Leu	His	Tyr		
5			CGC Arg														į	536
10			CTG Leu 165															584
15			GAG Glu														•	632
15			GCA Ala														6	680
20			GAG Glu														7	728
25			GTG Val														7	776
30			ATT Ile 245													CAG . Gln	8	324
			GAG Glu														8	372
35			CTC Leu														g	920

	CGG	GCC	ACA	TTT	GCC	AGC	CAC	GTG	CAG	CCT	GGC	CAG	TAC	GTG	CTG	GTG	968
	Arg	Ala	Thr	Phe	Ala 295	Ser	His	Val	Gln	Pro 300	Gly	Gln	Tyr	Val	Leu 305	Val	
5															TCT Ser		1016
				310					315					320			
10															ACA		1064
10	птэ	val	325	цец	GIY	ALG.	ıyı	330	FIO	Бец	1111	туз	335	GIĄ	Thr	Leu	
	GTG	GTG	GAG	GAT	GTG	GTG	GCA	TCC	TGC	TTC	GCG	GCC	GTG	GCT	GAC	CAC	1112
15	Val	Val 340	Glu	Asp	Val	Val	Ala 345	Ser	Cys	Phe	Ala	Ala 350	Val	Ala	Asp	His	
	CAC	CTG	GCT	CAG	TTG	GCC	TTC	TGG	CCC	CTG	AGA	CTC	ттт	CAC	AGC	TTG	1160
	Hi.s 355	Leu	Ala	Gln	Leu	Ala 360	Phe	Trp	Pro	Leu	Arg 365	Leu	Phe	His	Ser	Leu 370	
20	223					300					505					370	
	GCA	TGG	GGC	AGC	TGG	ACC.	·CCG	GGG	GAG	GGT	GТG	CAT	TGG	TAC	CCC	CAG	1208
	Ala	Trp	Gly	Ser	Trp 375	Thr	Pro	Gly	Glu	Gly 380	Val	His	Trp	Tyr	Pro 385	Gln	
25	CTG	CTC	TAC	CGC	CTG	GGG	CGT	СТС	CTG	СТА	GAA	GAG	GGC	AGC	TTC	CAC	1256
	Leu	Leu	Tyr	Arg 390	Leu	Gly	Arg	Leu	Leu 395	Leu	Glu	Glu	Gly	Ser 400	Phe	His	
	CCA	CTG	GGC	ATG	TCC	GGG	GCA	GGG	AGC	TGA	AAGGA	ACT (CCAC	CGCT	GC		1303
30	Pro	Leu	Gly 405	Met	Ser	Gly	Ala	Gly 410	Ser								
	ССТО	CCTG	GAA (CTGCT	rgtac	CT GO	GTC	CAGAA	A GCC	СТСТС	CAGC	CAGO	GAGGG	GAG (CTGGC	CCCTGG	1363
35	AAGO	GAC(CTG A	AGCTO	GGGG	GA CA	ACTGO	GCTCC	C TGC	CCATO	CTCC	TCTO	GCCA:	rga <i>i</i>	AGATA	ACACCA	1423
	TTGA	AGACT	TTG A	ACTGO	GGCAA	AC AC	CCAGO	CGTCC	c ccc	CACCO	CGCG	TCGT	rggto	GTA (GTCAT	TAGAGC	1483
	TGC	AAGCI	rga (GCTGC	GCGAC	GG GC	SATGO	STTGT	TGF	ACCCC	CTCT	CTCC	CTAGA	AGA (CCTTC	SAGGCT	1543

	GGC	ACGG(CGA (CTCC	CAAC!	rc ac	GCCT	GCTCT	г са	CTAC	GAGT	TTT	CATA	CTC 7	rgcc	rcccc	С	1603
5	ATTGGGAGGG CCCATTCCC (2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1191 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear																1622	
3	(2)	INF	ORMA'	rion	FOR	SEQ	ID ì	: 8 : O <i>l</i>	:									
		(i.)								re								
10									_		•							
			•	•														
			(I) T(OPOLO	OGY:	line	ear										
		(ii)	MOI	LECUI	LE T	YPE:	cDNA	A										
15																		
		, , , , ,	. זייריז	ATURI	٠.													
		(IX.				KEY:	CDS											
			•	•			1	1191										
20																		
		(xi)	SEÇ	QUENC	CE DE	ESCRI	IPTIO	ON: S	SEQ :	ID N	2:8:							
	ATG	GCT	CTC	CTG	ACC	AAT	СТА	CTG	CCC	TTG	TGC	TGC	TTG	GCA	CTT	CTG		48
25	Met	Ala	Leu	Leu	Thr	Asn	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu		
	1				5					10					15			
	~~~	am.a								000	999	000	ana	ći m m	600	000		0.6
								GGG Gly										96
30	Ата	ьеи	FIO	20	GIII	Set	СуЗ	GIY	25	GIĀ	ALG	GIĀ	110	30	Gry	Alg		
				_•														
	CGC	CGC	TAT	GCG	CGC	AAG	CAG	CTC	GTG	CCG	CTA	CTC	TAC	AAG	CAA	TTT		144
	Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe		
			35					40					45					
35																		
								ACC										192
	Val		Gly	Val	Pro	Glu		Thr	Leu	Gly	Ala		Gly	Pro	Ala	Glu		
		50					55					60						

	GGG	AGG	GTG	GCA	AGG	GGC	TCC	GAG	CGC	TTC	CGG	GAC	CTC	GTG	CCC	AAC	240
	Gly 65	Arg	Val	Ala	Arg	Gly 70	Ser	Glu	Arg	Phe	Arg 75	Asp	Leu	Val	Pro	Asn 80	
5	TAC	AAC	CCC	GAC	ATC	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGT	GGA	GCC	GAC	288
	Tyr	Asn	Pro	Asp	Ile 85	Ile	Phe	Lys	Asp	Glu 90	Glu	Asn	Ser	Gly	Ala 95	Asp	
	CGC	CTG	ATG	ACC	GAG	CGT	TGC	AAG	GAG	AGG	GTG	AAC	GCT	TTG	GCC	ATT	336
10	Arg	Leu	Met	Thr 100	Glu	Arg	Cys	Lys	Glu 105	Arg	Val	Asn	Ala	Leu 110	Ala	Ile	
	GCC	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTG	CGC	СТА	CGA	GTG	ACT	GAG	GGC	384
15	Ala	Val	Met 115	Asn	Met	Trp	Pro	Gly 120	Val	Arg	Leu	Arg	Val 125	Thr	Glu	Gly	
	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCT	CAG	GAT	TCA	CTC	CAC	TAC	GAA.	GGC	432
	Trp	Asp 130	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu 140	His	Tyr	Glu	Gly	
20																	
	CGT	GCT	TTG	GAC	ATC	ACT	ACG	TCT	GAC	CGC	GAC	CGC	AAC	AAG	TAT	GGG	480
	Arg 145	Ala	Leu	Asp	Ile	Thr 150	Thr	Ser	Asp	Arg	Asp 155	Arg	Asn	Lys	Tyr	Gly 160	
25	TTG	CTG	GCG	CGC	CTC	GCA	GTG	GAA	GCC	GGC	TTC	GAC	TGG	GTC	TAC	TAC	528
	Leu	Leu	Ala	Arg	Leu 165	Ala	Val	Glu	Ala	Gly 170	Phe	Asp	Trp	Val	Tyr 175	Tyr	
	GAG	TCC	CGC	AAC	CAC	GTC	CAC	GTG	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
30	Glu	Ser	Arg	Asn 180	His	Val	His	Val	Ser 185	Val	Lys	Ala	Asp	Asn 190	Ser	Leu	
	GCG	GTC	CGG	GCG	GGC	GGC	TGC	TTT	CCG	GGA	AAT	GCA	ACT	GTG	CGC	CTG	624
35	Ala	Val	Arg 195	Ala	Gly	Gly	Cys	Phe 200	Pro	Gly	Asn	Ala	Thr 205	Val	Arg	Leu	
	TGG	AGC	GGC	GAG	CGG	AAA	GGG	CTG	CGG	GAA	CTG	CAC	CGC	GGA	GAC	TGG	672
	Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	

	C TT TT	mmC	CCC	CCC	GAT	CCC	$T \subset X$	CCC	CCC	CTC	стс	CCC	NCC.	CCC	CTC	CTC	720
					Asp												720
		ьeu	АІА	Ala	ASP	230	ser	СТУ	Arg	vaı	235	FLO	TILL	FIO	vaı	240	
5	225					230					233					240	
3	CMC	mmc	CITIC	CAC	CGG	CAC	mmC	CAC	CCC	CCC	CCT	ጥር እ	no con en	CTC	CCT	CTC	768
																	700
	Leu	Pne	Leu	Asp	Arg	Asp	Leu	GIN	Arg	-	Ala	ser	Pne	vaı		vaı	
					245					250					255		
10	GAG	ACC	GAG	ፐርር	CCT	CCA	CGC	AAA	CTG	TТG	СТС	ACG	·CCC	TGG	CAC	CTG	816
					Pro												
	0_0		014	260				-10	265					270			
				200					200					2.0			
	GTG	TTT	GCC	GCT	CGA	GGG	CCG	GCG	CCC	GCG	CCA	GGC	GAC	ттт	GCA	CCG	864
15	·Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
			275					280					285				
	GTG	TTC	GCG	CGC	CGG	CTA	CGC	GCT	GGG	GAC	TCG	GTG	CTG	GCG	CCC	GGC	912
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	
20		290					295					300					
.*	GGG	GAT	GCG	CTT	CGG	CCA	GCG	CGC	GTG	GCC	CGT	GTG	GCG	CGG	GAG	GAA	960
	Gly	Asp	Ala	Leu	Arg	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	GJ.u	
	305					310					315					320	
25																	
	GCC	GTG	GGC	GTG	TTC	GCG	CCG	CTC	ACC	GCG	CAC	GGG	ACG	CTG	CTG	GTG	1008
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val	
					325					330					335		
30	AAC	GAT	GTC	CTG	GCC	TCT	TGC	TAC	GCG	GTT	CTG	GAG	AGT	CAC	CAG	TGG	1056
	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp	
				340					345					350			
25					TTT												1104
35	Ата	HlS	_	Ата	Phe	Ala	Pro		Arg	Leu	Leu	HIS		Leu	GIY	Ala	
			355					360					365				
	CTC	CTC	ccc	ccc	ccc	ccc	CTC	CNC	ccc	л С m	ccc	አጥ <u></u> ሮ	~ n m	TCC	<b>ጥ</b> እ <i>C</i>	TOT	1150
					GGG												1152
	ьeu	Leu	Pro	σтλ	Gly	нта	val	GIN			_	Met	UTS	ттр	тÀт	261	
										26/61							

370 375 380 CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CTG GGC TG 1191 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly 385 (2) INFORMATION FOR SEQ ID NO:9: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both 15 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA 20 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..1248 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: ATG GAC GTA AGG CTG CAT CTG AAG CAA TTT GCT TTA CTG TGT TTT ATC 48 Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile 1 5 10 15 30 AGC TTG CTT CTG ACG CCT TGT GGA TTA GCC TGT GGT CCT GGT AGA GGT 96 Ser Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly 20 25 30 35 TAT GGA AAA CGA AGA CAC CCA AAG AAA TTA ACC CCG TTG GCT TAC AAG 144 Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys 35 40 45 CAA TTC ATC CCC AAC GTT GCT GAG AAA ACG CTT GGA GCC AGC GGC AAA 192

27/61

P. Part

	Gln	Phe 50	Ile	Pro	Asn	Val	Ala 55	Glu	Lys	Thr	Leu	Gly 60	Ala	Ser	Gly	Lys	
	TAC	GAA	GGC	AAA	ATC	ACA	AGG	AAT	TCA	GAG	AGA	ттт	AAA	GAG	CTG	ATT	240
5	Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Ile	
	65					70					75					80	
	CCG	AAT	TAT	AAT	CCC	GAT	ATC	ATC	TTT	AAG	GAC	GAG	GAA	AAC	ACA	AAC	288
	Pro	Asn	Tyr	Asn		Asp	Ile	Ile	Phe	_	Asp	Glu	Glu	Asn		Asn	
10					85					90					95		
	GCT	GAC	AGG	CTG	ATG	ACC	AAG	CGC	TGT	AAG	GAC	AAG	TTA	AAT	TCG	TTG	336
	Ala	Asp	Arg	Leu	Met	Thr	Lys	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	
				100					105					110			
15	000	70 (17) 70	moo.		n m.c	770	C T C	m.c.c	000	CCC	CMC	70 70 70	CMC	ccc	CMC	л С П	204
				GTC Val													384
	mu		115	vai	1100	11011	1110	120		O L J	• • • •	270	125	11.2 9	•		
20	GAA	GGC	TGG	GAT	GAG	GAT	GGT	CAC	CAT	ATT	GAA	GAA	TCT	TTG	CAC	TAT	432
	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Leu	Glu	Glu	Ser	Leu	His	Tyr	
		130					1.35					140					
	GAG	GGA	CGG	GCA	GTG	GAC	ATC	ACT	ACC	TCA	GAC	AGG	GAT	AAA	AGC	AAG	480
25	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	
	145					150					155					160	
				CTA													528
30	Tyr	-GT À	Met	Leu	165	Arg	Leu	Ala	vaı	170	Ата	GIA	Pne	Asp	175	vaı	
50					100					1,0					175		
	TAT	TAT	GAA	TCT	AAA	GCC	CAC	ATA	CAC	TGC	TCT	GTC	AAA	GCA	GAA	AAT	576
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	
				180					185					190			
35																	
				GCT													624
	Ser	Val		Ala	Lys	Ser	Gly	_	Cys	Phe	Pro	Gly		Gly	Thr	Val	
			195					200					205				

						ACG											672
	Thr		Gly	Asp	Gly	Thr	-	Lys	Pro	Ile	Lys		Leu	Lys	Val	Gly	
		210					215					220					
5						GCA											720
	-	Arg	Val	Leu	Ala	Ala	Asp	Glu	Lys	Gly		Val	Leu	Ile	Ser	Ī	
	225					230					235					240	
			7.00		707	G 7 G	07.0	02 F	000	7.07	7.00	70 (70	n c c	() D D	mmc	7 m.c	7.00
10						GAC											768
10	Pne	TTE	мес	Pne		Asp	нтѕ	Asp	PIG		1111	Arg	Arg	GIII	255	iie .	
					245					250					255		•
	ርጥር	Δ T C	GAG	ACG	ጥር ል	GAA	ССТ	ጥጥር	ACC	ΔΔG	CTC	ACC	ርፐር	аст	GCC	GCG	816
						Glu											010
15	, , ,	110	014	260	552	010		2110	265	_10				270			
				200													
	CAC	CTA	GTT	TTC	GTT	GGA	AA:C	TCT	TCA	GCA	GCT	TCG	GGT	ATA	ACA	GCA	864
	His	Leu	Val	Phe	Val	Gly	Asn	Ser	Ser	Ala	Ala	Ser	Gly	Ile	Thr	Ala	
			275					280					285				
20												•					
	ACA	TTT	GCC	AGC	AAC	GTG	AAG	CCT	GGA	GAT	ACA	GTT	TTA	GTG	TGG	GAA	912
	Thr	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Asp	Thr	Val	Leu	Val	Trp	Glu	
		290					295					300					
25	GAC	ACA	TGC	GAG	AGC	CTC	AAG	AGC	GTT	ACA	GTG	AAA	AGG	ATT	TAC	ACT	960
	Asp	Thr	Cys	Glu	Ser	Leu	Lys	Ser	Val	Thr	Val	Lys	Arg	Ile	Tyr	Thr	
	305					310					315					320	
	GAG	GAG	CAC	GAG	GGC	TCT	TTT	GCG	CCA	GTC	ACC	.GCG	CAC	GGA	ACC	ATA	1008
30	Glu	Glu	His	Glu	Gly	Ser	Phe	Ala	Pro	Val	Thr	Ala	His	Gly	Thr	Ile	
					325					330					335		
						TTG											1056
	Ile	Val	Asp		Val	Leu	Ala	Ser		Tyr	Ala	Val	Ile		Asn	His	
35				340					345					350			
	7.7.	m.c. ~	~~-	~-	m.c.c	~~~		000	000	OF 6'	7.00	mm C	m¢m	~ ~	3 T C	O.T.C	1104
						GCT											1104
	ьys	Trp		HlS	Trp	Ala	rne		rro	val	arg	ьeu		nls	гуѕ	ьеи	
			355					360					365				

	ATG	ACG	TGG	CTT	TTT	CCG	GCT	CGT	GAA	TCA	AAC	GTC	AAT	TTT	CAG	GAG	1152
	Met	Thr	Trp	Leu	Phe	Pro	Ala	Arg	Glu	Ser	Asn	Val	Asn	Phe	Gln	Glu	
		370					375					380					
5	C A III	CCT	71.00	CAC	mcc	መክሮ	m C N	70.70	ATG	CTTC	መመጥ	CAC	አ መረግ	CCC	TI CT	TCC	1200
									Met								1200
	385	O ₁	110	1120	111	390	DCI	11511	1100	Dea	395	1110	1.10	O. J	001	400	
10	CTG	CTG	GAC	AGA	GAC	TCT	TTC	CAT	CCA	CTC	GGG	ATT	TTA	CAC	TTA	AGT	1248
	Leu	Leu	Asp	Arg	Asp	Ser	Phe	His	Pro	Leu	Gly	Ile	Leu	His	Leu	Ser	
					405					410					415		
	m G 7																1051
15	TGA																1251
15																	
	(2)	INFO	ORMAT	rion	FOR	SEQ	ID 1	NO:10	):								•
			(i) S						rics								
20									ino a								
								o aci linea				:					
				(0)	101	ОПОС	<b>31.</b> 1	LINE	21								
		( i	Li) N	40LEC	CULE	TYPE	E: pı	rotei	in								
25										,							
		( 2		SEQUE	ENCE	DESC	CRIPT	CION:	SEÇ	Q ID	NO:	10:					
•	Mot	V a l	Glu	Mo+	Len	T.011	T.011	Thr	Arg	Tla	T. 0.1	T.A.I.	Val	Glv	Pho	TlΔ	
30	1	Val	Gru	1100.	5	пси	БСС	1111	rirg	10	БСС	шси	Vai	CILY	15	110	
	Cys	Ala	Leu	Leu	Val	Ser	Ser	Gly	Leu	Thr	Cys	Gly	Pro	Gl.y	Arg	Gly	
				20					25					30			
35	Ile	Gly		Arg	Arg	His	Pro		Lys	Leu	Thr	Pro		Ala	Tyr	Lys	
35	Ile	Gly	Lys 35	Arg	Arg	His	Pro	Lys 40	Lys	Leu	Thr	Pro	Leu 45	Ala	Tyr	Lys	
35			35					40					45				
35			35					40	Lys				45				

30/61

	Tyr 65	Glu	Gly	Lys	Ile	Thr 70	Arg	Asn	Ser	Glu	Arg 75	Phe	Lys	Glu	Leu	Thr 80
5	Pro	Asn	Tyr	Asn	Pro 85	Asp	Ile	Ile	Phe	Lys 90	Asp	Glu	Glu	Asn	Thr 95	Gly
10	Ala	Asp	Arg	Leu 100	Met	Thr	Gln	Arg	Cys 105	Lys	Asp	Lys	Leu	Asn 110	Ala	Leu
	Ala	Ile	Ser 115	Val	Met	Asn	Gln	Trp 120	Pro	Gly	Val	Lys	Leu 125	Arg	Val	Thr
15	Glu	Gly 130	Trp	Asp	Glu	Asp	Gly 135	His	His	Ser	Glu	Glu 140	Ser	Leu	Hi.s	Туг
	Glu 145	Gly	Arg	Ala	Val	Asp 150	Ile	Thr	Thr	Ser	Asp 155	Arg	Asp	Arg	Ser	Lys 160
20	Tyr	Gly	Met	Leu	Ala 165	Arg	Leu	Ala	Val	Glu 170	Ala	Gly	Phe	Asp	Trp 175	Val
25	Tyr	Tyr	Glu	Ser 180	Lys	Ala	His	Ile	His 185	Cys	Ser	Val	Lys	Ala 190	Glu	Asn
23	Ser	Val	Ala 195	Ala	Lys	Ser	Gly	Gly 200	Cys	Phe	Pro	Gly	Ser 205	Ala	Thr	Val
30	His	Leu 210	Glu	His	Gly	Gly	Thr 215	Lys	Leu	Val	Lys	Asp 220	Leu	Ser	Pro	Gly
	Asp 225	Arg	Val	Leu	Ala	Ala 230	Asp	Ala	Asp	Gly	Arg 235	Leu	Leu	Tyr	Ser	Asp 240
35	Phe	Leu	Thr	Phe	Leu 245	Asp	Arg	Met	Asp	Ser 250	Ser	Arg	Lys	Leu	Phe 255	Tyr
	Val	Ile	Glu	Thr 260	Arg	Gln	Pro	Arg	Ala 265	Arg	Leu	Leu	Leu	Thr 270	Ala	Ala

15

25

His	Leu	Leu	Phe	Val	Ala	Pro	Gln	His	Asn	Gln	Ser	Glu	Ala	Thr	Gly
		275					280					285			

- 5 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln 290 295 300
  - Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser 305 310 315 320

Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro 325 330 335

Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys

340 345 350

Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro 355 360 365

20 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala 370 375 380

Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg 385 390 395 400

Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
405 410 415

Pro Leu Gly Met Val Ala Pro Ala Ser 30 420 425

#### (2) INFORMATION FOR SEQ ID NO:11:

- 35 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 396 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

# (ii) MOLECULE TYPE: protein

5		(2	xi) :	SEQUI	ENCE	DES	CRIP'	rion	: SE	Q ID	NO:11:					
	Met 1	Ala	Leu	Pro	Ala 5	Ser	Leu	Leu	Pro	Leu 10	Cys	Суѕ	Leu	Ala	Leu 15	Leu
10	Ala	Leu	Ser	Ala 20	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val 30	Gly	Arg
15	Arg	Arg	Tyr 35	Val	Arg	Lys	Gln	Leu 40	Val	Pro	Leu	Leu	Tyr 45	Lys	Gln	Phe
13	Val	Pro 50	Ser	Met	Pro	Glu	Arg 55	Thr	Leu	Gly	Ala	Ser 60	Gly	Pro	Ala	Glu
20	Gly 65	Arg	Val	Thr	Arg	Gly 70		Glu	Arg	Phe	Arg 75	Asp	Leu	Val	Pro	Asn 80
	Tyr	Asn	Pro	Asp	Ile 85	Ile	Phe	Lys	Asp	Glu 90	Glu	Asn	Ser	Gly	Ala 95	Asp
25	Arg	Leu	Met	Thr 100	Glu	Arg	Cys	Lys	Glu 105	Arg	Val	Asn	Ala	Leu 110	Ala	Ile
20	Ala	Val	Met 115	Asn	Met	Trp	Pro	Gly 120	Val	Arg	Leu	Arg	Val 125	Thr	Glu	Gly
30	Trp	Asp 130	Glu	Asp	Gly	His	His 135	Ala	Gln	Asp	Ser	Leu 140	His	Tyr	Glu	Gly
35	Arg 145	Ala	Leu	Asp	Ile	Thr 150	Thr	Ser	Asp	Arg	Asp 155	Arg	Asn	Lys	Tyr	Gly 160
	Leu	Leu	Ala	Arg	Leu 165	Ala	Val	Glu	Ala	Gly 170	Phe	Asp	Trp	Val	Tyr 175	Tyr

	Glu	Ser	Arg	Asn 180	His	Ile	His	Val	Ser 185	Val	Lys	Ala	Asp	Asn 190	Ser	Leu
5	Ala	Val	Arg 195	Ala	Gly	Gly	Cys	Phe 200	Pro	Gly	Asn	Ala	Thr 205	Val	Arg	Leu
	Arg	Ser 210	Gly	Glu	Arg	Lys	Gly 215	Leu	Arg	Glu	Leu	His 220	Arg	Gly	Asp	Trp
10	Val 225	Leu	Ala	Ala	Asp	Ala 230	Ala	Gly	Arg	Val	Val 235	Pro	Thr	Pro	Val	Leu 240
15	Leu	Phe	Leu	Asp	Arg 245	Asp	Leu	Gln	Arg	Arg 250	Ala	Ser	Phe	Val	Ala 255	Val
13	Glu	Thr	Glu	Arg 260	Pro	Pro	Arg	Lys	Leu 265	Leu	Leu	Thr	Pro	Trp 270	His	Leu
20	Val	Phe	Ala 275	Ala	Arg	Gly	Pro	Ala 280	Pro	Ala	Pro	Gly	Asp 285	Phe	Ala	Pro
	Val	Phe 290	Ala	Arg	Arg	Leu	Arg 295	Ala	Gly	Asp	Ser	Val 300	Leu	Ala	Pro	Gly
25	Gly 305	Asp	Ala	Leu	Gln	Pro 310	Ala	Arg	Val	Ala	Arg 315	Val	Ala	Arg	Glu	Glu 320
30	Ala	Val	Gly	Val	Phe 325	Ala	Pro	Leu	Thr		His	_	Thr	Leu	Leu 335	
	Asn	Asp	Val	Leu 340	Ala	Ser	Cys	Tyr	Ala 345	Val	Leu	Glu	Ser	His 350	Gln	Trp
35	Ala	His	Arg 355	Ala	Phe	Ala	Pro	Leu 360	Arg	Leu	Leu	His	Ala 365	Leu	Gly	Ala
	Leu	Leu 370	Pro	Gly	Gly	Ala	Val 375	Gln	Pro	Thr	Gly	Met 380	His	Trp	Tyr	Ser

10

15

20

25

30

35

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly 385 390 395 (2) INFORMATION FOR SEQ ID NO:12: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 411 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu 10 Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg 20 25 30 Val Val Gly Ser Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala 35 40 45 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser 50 55 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu 70 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn 90 95 85 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn 100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg

35/61

Ĭ

			115					120					125			
5	Val	Thr 130	Glu	Gly	Arg	Asp	Glu 135	Asp	Gly	His	His	Ser 140	Glu	Glu	Ser	Leu
J	His 145	Tyr	Glu	Gly	Arg	Ala 150	Val	Asp	Ile	Thr	Thr 155	Ser	Asp	Arg	Asp	Arg 160
10	Asn	Lys	Tyr	Gly	Leu 165	Leu	Ala	.Arg	Leu	Ala 170	Val	Glu	Ala	Gly	Phe 175	Asp
	Trp	Val	Tyr	Tyr 180	Glu	Ser	Lys	Ala	His 185	Val	His	Суз	Ser	Val 190	Lys	Ser
15	Glu	His	Ser 195	Ala	Ala	Ala	Lys	Thr 200	Gly	Gly	Cys	Phe	Pro 205	Ala	Gly	Ala
20	Gln	Val 210	Arg	Leu	Glu	Asn	Gly 215	Glu	Arg	Val	Ala	Leu 220	Ser	Ala	Val	Lys
	Pro 225	Gly	Asp	Arg	Val	Leu 230	Ala	Met	Gly	Glu	Asp 235	Gly	Thr	Pro	Thr	Phe 240
25	Ser	Asp	Val	Leu	Ile 245	Phe	Leu	Asp	Arg	Glu 250	Pro	Asn	Arg	Leu	Arg 255	Ala
	Phe	Gln	Val	Ile 260	Glu	Thr	Gln	Asp	Pro 265	Pro	Arg	Arg	Leu	Ala 270	Leu	Thr
30	Pro	Ala	His 275	Leu	Leu	Phe	Ile	Ala 280	Asp	Asn	His	Thr	Glu 285	Pro	Ala	Ala
35	His	Phe 290	Arg	Ala	Thr	Phe	Ala 295	Ser	His	Val	Gln	Pro 300	Gly	Gln	Tyr	Val
	Leu 305	Val	Ser	Gly	Val	Pro 310	Gly	Leu	Gln	Pro	Ala 315	Arg	Val	Ala	Ala	Val 320
	Ser	Thr	His	Val	Ala	Leu	Gly	Ser	Tyr	Ala 36/61		Leu	Thr	Arg	His	Gly

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser (2) INFORMATION FOR SEQ ID NO:13: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 437 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: Met Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly 

Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe

37/61

1.

			35					40					45			
5	Ile	Pro 50	Asn	Val	Ala	Glu	Lys 55	Thr	Leu	Gly	Ala	Ser 60	Gly	Arg	Tyr	Glu
3	Gly 65	Lys	Ile	Thr	Arg	Asn 70	Ser	Glu	Arg	Phe	Lys 75	Glu	Leu	Thr	Pro	Asn 80
10	Tyr	Asn	Pro	Asp	Ile 85	Ile	Phe	Lys	Asp	Glu 90	Glu	Asn	Thr	Gly	Ala 95	Asp
	Arg	Leu	Met.	Thr 100	Gln	Arg	Cys	Lys	Asp 105	Lys	Leu	Asn	Ala	Leu 110	Ala	Ile
15	Ser	Val	Met 115	Asn	Gln	Trp	Pro	Gly 120	Val	Arg	Leu	Arg	Val 125	Thr	Glu	Gly
20	Trp	Asp	Glu	Asp	Gly	His	His 135	Ser	Glu	Glu	Ser	Leu 140	His	Tyr	Glu	Gly
-	Arg 145	Ala	Val	Asp	Ile	Thr 150	Thr	Ser	Asp	Arg	Asp 155	Arg	Ser	Lys	Tyr	Gly 160
25	Met	Leu	Ala	Arg	Leu 165	Ala	Val	Glu	Ala	Gly 170	Phe	Asp	Trp	Val	Tyr 175	Туr
	Glu	Ser	Lys	Ala 180	His	Ile	His	Cys	Ser 185	Val	Lys	Ala	Glu	Asn 190	Ser	Val
30	Ala	Ala	Lys 195	Ser	Gly	Gly	Cys	Phe 200	Pro	Gly	Ser	Ala	Thr 205	Val	His	Leu
35	Glu	Gln 210	Gly	Gly	Thr	Lys	Leu 215	Val	Lys	Asp	Leu	Arg 220	Pro	Gly	Asp	Arg
	Val 225	Leu	Ala	Ala	Asp	Asp 230	Gln	Gly	Arg	Leu	Leu 235	Tyr	Ser	Asp	Phe	Leu 240
	Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys 38/61	_	Val	Phe	Tyr	Val	Ile

					245	•				250					255	
5	Glu	Thr	Leu	Glu 260	Pro	Arg	Glu	Arg	Leu 265	Leu	Leu	Thr	Ala	Ala 270	His	Leu
J	Leu	Phe	Val 275	Ala	Pro	His	Asn	Asp 280	Ser	Gly	Pro	Thr	Pro 285	Gly	Pro	Ser
10	Ala	Leu 290	Phe	Ala	Ser	Arg	Val 295	Arg	Pro	Gly	Gln	Arg 300	Val	Tyr	Val	Val
	Ala 305	Glu	Arg	Gly	Gly	Asp 310	Arg	Arg	Leu	Leu	Pro 315	Ala	Ala	Val	His	Ser 320
15	Val	Thr	Leu	Arg	Glu 325	Glu	Glu	Ala	Gly	Ala 330	Tyr	Ala	Pro	Leu	Thr 335	Ala
20	His	Gly	Thr	Ile 340	Leu	Ile	Asn	Arg	Val 345	Leu	Ala	Ser	Cys	Tyr 350	Ala	Val
	Ile	Glu	Glu 355	His	Ser	Trp	Ala	His 360	Arg	Ala	Phe	Ala	Pro 365	Phe	Arg	Leu
25	Ala	His 370	Ala	Leu	Leu	Ala	Ala 375	Leu	Ala	Pro	Ala	Arg 380	Thr	Asp	Gly	Gly
	Gly 385	Gly	Gly	Ser	Ile	Pro 390	Ala	Ala	Gln	Ser	Ala 395	Thr	Glu	Ala	Arg	Gly 400
30	Ala	Glu	Pro	Thr	Ala 405	Gly	Ile	His	Trp	Tyr 410	Ser	Gln	Leu	Leu	Tyr 415	His
35	Ile	Gly	Thr	Trp 420	Leu	Leu	Asp	Ser	Glu 425	Thr	Met	His	Pro	Leu 430	Gly	Met
	Ala	Val	Lys 435	Ser	Ser											

## (2) INFORMATION FOR SEQ ID NO:14:

(A) LENGTH: 418 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

15

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser

1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

20 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile 35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly 50 55 60

25

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
30 85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
100 105 110

35 Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp 115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg 130 135 140

40/61

	Ala 145	Val	Asp	Ile	Thr	Thr 150	Ser	Asp	Arg	Asp	Lys 155	Ser	Lys	Tyr	Gly	Thr 160
5	Leu	Ser	Arg	Leu	Ala 165	Val	Glu	Ala	Gly	Phe 170	Asp	Trp	Val	Tyr	Tyr 175	Glu
10	Ser	Lys	Ala	His 180	Ile	His	Cys	Ser	Val 185	Lys	Ala	Glu	Asn	Ser 190	Val	Ala
10	Ala	Lys	Ser 195	Gly	Gly	Cys	Phe	Pro 200	Gly	Ser	Ala	Leu	Val 205	Ser	Leu	Gln
15	Asp	Gly 210	Gly	Gln	Lys	Ala	Val 215	Lys	Asp	Leu	Asn	Pro 220	Gly	Asp	Lys	Val
	Leu 225	Ala	Ala	Asp	Ser	Ala 230	Gly	Asn	Leu	Val	Phe 235	Ser	Asp	Phe	Ile	Met 240
20	Fhe	Thr	Asp	Arg	Asp 245	Ser	Thr	Thr	Arg	Arg 250	Val	Phe	Tyr	Val	Ile 255	Glu
	Thr	Gln	Glu	Pro 260	Val	Glu	Lys	Ile	Thr 265	Leu	Thr	Ala	Ala	His 270	Leu	Leu
25	Phe	Val	Leu 275	Asp	Asn	Ser	Thr	Glu 280	Asp	Leu	His	Thr	Met 285	Thr	Ala	Ala
30	Tyr	Ala 290	Ser	Ser	Val	Arg	Ala 295	Gly	Gln	Lys	Val	Met 300	Val	Val	Asp	Asp
	Ser 305	Gly	Gln	Leu	Lys	Ser 310	Val	Ile	Val	Gln	Arg 315	Ile	Tyr	Thr	Glu	Glu 320
35	Gln	Arg	Gly	Ser	Phe	Ala	Pro	Val	Thr	Ala 330	His	Gly	Thr	Ile	Val 335	Val
	Asp	Arg	Ile	Leu 340	Ala	Ser	Cys	Tyr	Ala 345	Val	Ile	Glu	Asp	Gln 350	Gly	Leu

	Ala	His	Leu 355	Ala	Phe	Ala	Pro	360	Arg	Leu	Tyr	Tyr	Tyr 365	Val	Ser	Ser
5	Phe	Leu 370	Ser	Pro	Lys	Thr	Pro 375	Ala	Val	Gly	Pro	Met 380	Arg	Leu	Tyr	Asn
10	Arg 385	Arg	Gly	Ser	Thr	Gly 390	Thr	Pro	Gly	Ser	Cys 395	His	Gln	Met	Gly	Thr 400
10	Trp	Leu	Leu	Asp	Ser 405	Asn	Met	Leu	His	Pro 410	Leu	Gly	Met	Ser	Val 415	Asn
15	Ser	Ser														
	(2)	INFO	ORMA	rion	FOR	SEQ	ID 1	NO:15	ō:							
20			(i) S	(A)		NGTH:	: 475 amino	am:			3					
25		. (:	ii) M	40LE0	CULE	TYPI	E: pı	rotei	in							
30		(2	<i) \$<="" th=""><th>SEQUE</th><th>ENCE</th><th>DESC</th><th>CRIPT</th><th>rion:</th><th>: SE(</th><th>) ID</th><th>NO:</th><th>15:</th><th></th><th></th><th></th><th></th></i)>	SEQUE	ENCE	DESC	CRIPT	rion:	: SE(	) ID	NO:	15:				
	Met 1	Leu	Leu	Leu	Ala 5	Arg	Cys	Leu	Leu	Leu 10	Val	Leu	Val	Ser	Ser 15	Leu
35	Leu	Val	Cys	Ser 20	Gly	Leu	Ala	Cys	Gly 25	Pro	Gly	Arg	Gly	Phe 30	Gly	Lys

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile

40

35

	Pro	Asn 50	Val	Ala	Glu	Lys	Thr 55	Leu	Gly	Ala	Ser	Gly 60	Arg	Tyr	Glu	Gly
5	Lys 65	Ile	Ser	Arg	Asn	Ser 70	Glu	Arg	Phe	Lys	Glu 75	Leu	Thr	Pro	Asn	Tyr 80
	Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg
10	Leu	Met	Thr	Gln 100	Arg	Cys	Lys	Asp	Lys 105	Leu	Asn	Ala	Leu	Ala 110	Ile	Ser
15	Val	Met	Asn 115	Gln	Trp	Pro	Gly	Val 120	Lys	Leu	Arg	Val	Thr 125	Glu	Gly	Trp
	Asp	Glu 130	Asp	Gly	His	His	Ser 135	Glu	Glu	Ser	Leu	His 140	Tyr	Glu	Gly	Arg
20	Ala 145	Val	Asp	Ile	Thr	Thr 150	Ser	Asp	Arg	Asp	Arg 155	Ser	Lys	Tyr	Gly	Met 160
	Leu	Ala	Arg	Leu	Ala 165	Val	Glu	Ala	Gly	Phe 170	Asp	Trp	Val	Tyr	Tyr 175	Glu
25	Ser	Lys	Ala	His 180	Ile	His	Cys	Ser	Val 185	Lys	Ala	Glu	Asn	Ser 190	Val	Ala
30	Ala	Lys	Ser 195	Gly	Gly	Cys	Phe		Gly		Ala	Thr	Val 205	His	Leu	Glu
30	Gln	Gly 210	Gly	Thr	Lys	Leu	Val 215	Lys	Asp	Leu	Ser	Pro 220	Gly	Asp	Arg	Val
35	Leu 225	Ala	Ala	Asp	Asp	Gln 230	Gly	Arg	Leu	Leu	Tyr 235	Ser	Asp	Phe	Leu	Thr 240
	Phe	Leu	Asp	Arg	Asp 245	Asp	Gly	Ala	Lys	Lys 250	Val	Phe	Tyr	Val	Ile 255	Glu

	Thr	Arg	Glu	Pro 260	Arg	Glu	Arg	Leu	Leu 265	Leu	Thr	Ala	Ala	His 270	Leu	Leu
5	Phe	Val	Ala 275	Pro	His	Asn	Asp	Ser 280	Ala	Thr	Gly	Glu	Pro 285	Glu	Ala	Ser
	Ser	Gly 290	Ser	Gly	Pro	Pro	Ser 295	Gly	Gly	Ala	Leu	Gly 300	Pro	Arg	Ala	Leu
10	Phe 305	Ala	Ser	Arg	Val	Arg 310	Pro	Gly	Gln	Arg	Val 315	Tyr	Val	Val	Ala	Glu 320
15	Arg	Asp	Gly	Asp	Arg 325	Arg	Leu	Leu	Pro	Ala 330	Ala	Val	His	Ser	Val 335	Thr
	Leu	Ser	Glu	Glu 340	Ala	Ala	Gly	Ala	Tyr 345	Ala	Pro	Leu	Thr	Ala 350	Gln	Gly
20-	Thr	Ile	Leu 355	Ile	Asn	Ärg	Val	Leu 360	Ala	Ser	Cys	Туг	Ala 365	Val.	Ile	Glu
	Glu	His 370	Ser	Trp	Ala	His	Arg 375	Ala	Phe	Ala	Pro	Phe 380	Arg	Leu	Ala	His
25	Ala 385	Leu	Leu	Ala	Ala	Leu 390	Ala	Pro	Ala	Arg	.Thr 395	Asp	Arg	Gly	Gly	Asp
30	Ser	Gly	Gly	Gly	Asp 405	Arg	Gly	Gly	Gly	Gly 410	Gly	Arg	Val	Ala	Leu 415	Thr
30	Ala	Pro	Gly	Ala 420	Ala	Asp	Ala	Pro	Gly 425	Ala	Gly	Ala	Thr	Ala 430	Gly	Ile
35	His	Trp	Tyr 435	Ser	Gln	Leu	Leu	Tyr 440	Gln	Ile	Gly	Thr	Trp 445	Leu	Leu	Asp
	Ser	Glu 450	Ala	Leu	His	Pro	Leu 455	Gly	Met	Ala	Val	Lys 460	Ser	Ser	Xaa	Ser

10

.20

25

35

Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala 465 470 475 (2) INFORMATION FOR SEQ ID NO:16: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 411 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu 1 10 Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Fro Gly Arg 20 25 Val Val Gly Ser Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala 40 45 35 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser 50 55 60 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu 65 70 75 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn 85 90 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn 100 105 110 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg 120 125 115

45/61

Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala 255 . Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala 46/61

				340					345					350		
5	Asp	His	His 355	Leu	Ala	Gln	Leu	Ala 360	Phe	Trp	Pro	Leu	Arg 365	Leu	Phe	His
3	Ser	Leu 370	Ala	Trp	Gly	Ser	Trp 375	Thr	Pro	Gly	Glu	Gly 380	Val	His	Trp	Туг
10	Pro 385	Gln	Leu	Leu	Tyr	Arg 390	Leu	Gly	Arg	Leu	Leu 395	Leu	Glu	Glu	Gly	Ser 400
	Phe	His	Pro	Leu	Gly 405	Met	Ser	Gly	Ala	Gly 410	Ser					
15	(2)	INFO	ORMA'	rion	FOR	SEQ	ID 1	NO:1	7:							
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 amino acids															
	(A) LENGTH: 396 amino acids (B) TYPE: amino acid															
20				(D)	) TOI	POLO	GY: .I	linea	ar							
		( =	ii) ì	MOLEC	CULE	ТҮРІ	E: pi	rote	in							
25		( 2	ki) S	SEQUE	ENCE	DESC	CRIPT	CION:	: SE(	) ID	NO:	L7:				
25	Met 1	Ala	Leu	Leu	Thr 5	Asn	Leu	Leu	Pro	Leu 10	Cys	Cys	Leu	Ala	Leu 15	Leu
30	Ala	Leu	Pro	Ala 20	Gln	Ser	Cys	Gly	Pro 25	Gly	Arg	Gly	Pro	Val 30	Gly	Arg
	Arg	Arg	Tyr 35	Ala	Arg	Lys	Gln	Leu 40	Val	Pro	Leu	Leu	Tyr 45		Gln	Phe
35	Val	Pro 50	Gly	Val	Pro	Glu	Arg 55	Thr	Leu	Gly	Ala	Ser 60	Gly	Pro	Ala	Glu
	Gly 65	Arg	Val	Ala	Arg	Gly 70	Ser	Glu	Arg	Phe	Arg 75	Asp	Leu	Val	Pro	Asn 80

	Tyr	Asn	Pro	Asp	Ile 85	Ile	Phe	Lys	Asp	Glu 90	Glu	Asn	Ser	Gly	Ala 95	Asp
5	Arg	Leu	Met	Thr 100	Glu	Arg	Cys	Lys	Glu 105	Arg	Val	Asn	Ala	Leu 110	Ala	Ile
10	Ala	Val	Met 115	Asn	Met	Trp	Pro	Gly 120	Val	Arg	Leu	Arg	Val 125	Thr	Glu	Gly
10	Trp	Asp 130	Glu	Asp	Gly	His	His 135	Ala	Gln	Asp	Ser	Leu 140	His	Tyr	Glu	Gly
15	Arg 145	Ala	Leu	Asp	Ile	Thr 150	Thr	Ser	Asp	Arg	Asp 155	Arg	Asn	Lys	Tyr	Gly 160
	Leu	Leu	Al.a	Arg	Leu 165	Ala	Val	Glu	Ala	Gly 170	Phe	Asp	Trp	Val	Tyr 175	Tyr
20	Glu	Ser	Arg	Asn 180	His	Val	His	Val	Ser 185	Val	Lys	Ala	Asp	Asn 190	Ser	Leu
25	Ala	Val	Arg 195	Ala	Gly	Gly	Cys	Phe 200	Pro	Gly	Asn	Ala	Thr 205	Val	Arg	Leu
23	Trp	Ser 210	Gly	Glu	Arg	Lys	Gly 215	Leu	Arg	Glu	Leu	His 220	Arg	Gly	Asp	Trp
30	Val 225		Ala	Ala	Asp	Ala 230		Gly	Arg	Val		Pro		Pro	Val	Leu 240
	Leu	Phe	Leu	Asp	Arg 245	Asp	Leu	Gln	Arg	Arg 250	Ala	Ser	Phe	Val	Ala 255	Val
35	Glu	Thr	Glu	Trp 260	Pro	Pro	Arg	Lys	Leu 265	Leu	Leu	Thr	Pro	Trp 270	His	Leu
	Val	Phe	Ala 275	Ala	Arg	Gly	Pro	Ala 280	Pro	Ala	Pro	Gly	Asp 285	Phe	Ala	Pro

	Val	Phe 290	Ala	Arg	Arg	Leu	Arg 295	Ala	Gly	Asp	Ser	Val 300	Leu	Ala	Pro	Gly
5	Gly 305	Asp	Ala	Leu	Arg	Pro 310	Ala	Arg	Val	Ala	Arg 315	Val	Ala	Arg	Glu	Glu 320
10	Ala	Val	Gly	Val	Phe 325	Ala	Pro	Leu	Thr	Ala 330	His	Gly	Thr	Leu	Leu 335	Val
	Asn	Asp	Val	Leu 340	Ala	Ser	Cys	Tyr	Ala 345	Val	Leu	Glu	Ser	His 350	Gl'n	Trp
15	Ala	His	Arg 355	Ala	Phe	Ala	Pro	Leu 360	Arg	Leu	Leu	His	Ala 365	Leu	Gly	Ala
	Leu	Leu 370	Pro	Gly	Gly	Ala	Val 375	Gln	Pro	Thr	Gly	Met: 380	His	Trp	Tyr	Ser
20	Arg 385	Leu	Leu	Tyr	Arg	Leu 390	Ala	Glu	Glu	Leu	Leu 395	Gly				
25	(2)	INF	ORMA	rion	FOR	SEQ	ID 1	NO:18	3:							
			(i) S		LEI	NGTH	: 416	ERIST 6 ami	ino a		6					
30		*		(D)	тоі	POLO	GY: I	linea	ar							
							-	rotei TION:		Q ID	NO:	18:				
35		·	•													

49/61

10

15

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly

5

				20					25					30		
5	Tyr	Gly	Lys 35	Arg	Arg	His	Pro	Lys 40	Lys	Leu	Thr	Pro	Leu 45	Ala	Tyr	Lys
J	Gln	Phe 50	Ile	Pro	Asn	Val	Ala 55	Glu	Lys	Thr	Leu	Gly 60	Ala	Ser	Gly	Lys
10	Tyr 65	Glu	Gly	Lys	Ile	Thr 70	Arg	Asn	Ser	Glu	Arg 75	Phe	Lys	Glu	Leu	Ile 80
	.Pro	Asn	Tyr	Asn	Pro 85	Asp	Ile	Ile	Phe	Lys 90	Asp	Glu	Glu	Asn	Thr 95	Asn
1.5	Ala	Asp	Arg	Leu 100	Met	Thr	Lys	Arg	Cys 105	Lys	Asp	Lys	Leu	Asn 110	Ser	Leu
20	Ala	Ile	Ser 115	Va.l	Met	Asn	His	Trp 120	Pro	Gly	Val	Lys	Leu 125	Arg	Val	Thr
	Glu	Gly 130	Trp	Asp	Glu	Asp	Gly 135	His	His	Leu	Glu	Glu 140	Ser	Leu	His	Tyr
25	Glu 145	Gly	Arg	Ala	Val	Asp 150	Ile	Thr	Thr	Ser	Asp 155	Arg	Asp	Lys	Ser	Lys 160
	Tyr	Gly	Met	Leu	Ser 165	Arg	Leu	Ala	Val	Glu 170	Ala	Gly	Phe	Asp	Trp 175	Val
30	Tyr	Tyr	Glu	Ser 180	Lys	Ala	His	Ile	His 185	Cys	Ser	Val	Lys	Ala 190	Glu	Asn
35	Ser	Val	Ala 195	Ala	Lys	Ser	Gly	Gly 200	Cys	Phe	Pro	Gly	Ser 205	Gly	Thr	Val
	Thr	Leu 210	Gly	Asp	Gly	Thr	Arg 215	Lys	Pro	Ile	Lys	Asp 220	Leu	Lys	Val	Gly
	Asp	Arg	Val	Leu	Ala	Ala	Asp	Glu		Gly 50/61		Val	Leu	Ile	Ser	Asp

	225					230					235					240
5	Phe	Ile	Met	Phe	Ile 245	Asp	His	Asp	Pro	Thr 250	Thr	Arg	Arg	Gln	Phe 255	Ile
3	Val	Ile	Glu	Thr 260	Ser	Glu	Pro	Phe	Thr 265	Lys	Leu	Thr	Leu	Thr 270	Ala	Ala
10	His	Leu	Val 275	Phe	Val	Gly	Asn	Ser 280	Ser	Ala	Ala	Ser	Gly 285	Ile	Thr	Ala
	Thr	Phe 290	Ala	Ser	Asn	Val	Lys 295	Pro	Gly	.Asp	Thr	Val 300	Leu	Val	Trp	Glu
15	Asp 305	Thr	Cys	Glu	Ser	Leu 310	Lys	Ser	Val	Thr	Val 315	Lys	Arg	Ile	Tyr	Thr 320
20	Glu	Glu	His	Glu	Gly 325	Ser	Phe	Ala	Pro	Val 330		Ala	His	Gly	Thr 335	Ile
	Ile	Val	Asp	Gln 340	Val	Leu	Ala	Ser	Cys 345	Tyr	Ala	Val	Ile	Glu 350	Asn	His
25	Lys	Trp	Ala 355	His	Trp	Ala	Phe	Ala 360	Pro	Val	Arg	Leu	Cys 365	His	Lys	Leu
	Met	Thr 370	Trp	Leu	Phe	Pro	Ala 375	Arg	Glu	Ser	Asn	Val 380	Asn	Phe	Gln	Glu
30	Asp 385	Gly	Ile	His	Trp	Tyr 390	Ser	Asn	Met	Leu	Phe 395	His	Ile	Gly	Ser	Trp 400
35	Leu	Leu	Asp	Arg	Asp 405	Ser	Phe	His	Pro	Leu 410	Gly	Ile	Leu	His	Leu 415	Ser

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1416 base pairs

	(B) TYPE: nucleic acid																
			( (	C) S'	TRAN	DEDN	ESS:	bot	h								
			( )	D) T	OPOL	OGY:	lin	ear									
5																	
		(ii	) MO	LECU:	LE T	YPE:	cDN	Ą									
		(ix	) FE	ATUR	E:												
10			( )	A) N	AME/I	KEY:	CDS										
			(1	B) L	OCAT:	ION:	1	1413									
		(xi	) SE	QUEN	CE DI	ESCR:	IPTIC	: NC	SEQ :	ID N	0:19	:					
15																	
									TGG								48
		Asp	Asn	His		Ser	Val	Pro	Trp		Ser	Ala	Ala	Ser		Thr	
	1				5					10					15		
	m.o.m.	O.T. C.		C.T.C	aan	maa	~ n n	700	- 1 - C   T	~~~	mm.a	a. a	mm.c	G 7 G		07.0	0.6
20									CCA								96
	Cys	Leu	ser	20	GTÀ	Cys	GIII	Mer	Pro 25	GIII	PHe	GIII	Pne	30	Pne	GLII	
				20					2.5					30			
	СТС	CAA	ATC	CGC	AGC	GAG	CT'C	CAT	CTC	CGC	AAG	acc	GCA	AGA	AGA	ACG	144
25									Leu								
			35	,				40		,	4		45	.,	,		
	CAA	ACG	ATG	CGC	CAC	ATT	GCG	CAT	ACG	CAG	CGT	TGC	CTC	AGC	AĞG	CTG	192
	Gln	Thr	Met	Arg	His	Ile	Ala	His	Thr	Gln	Arg	Cys	Leu	Ser	Arg	Leu	
30		50					55					60					
	ACC	TCT	CTG	GTG	GCC	CTG	CTG	CTG	ATC	GTC	TTG	CCG	ATG	GTC	TTT	AGC	240
	Thr	Ser	Leu	Val	Ala	Leu	Leu	Leu	Ile	Val	Leu	Pro	Met	Val	Phe	Ser	
	65					70					75					80	
35																	
	CCG	GCT	CAC	AGC	TGC	GGT	CCT	GGC	CGA	GGA	TTG	GGT	CGT	CAT	AGG	GCG	288
	Pro	Ala	His	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Arg	His	Arg	Ala	
					85					90					95		

	CGC	AAC	CTG	TAT	CCG	CTG	GTC	CTC	AAG	CAG	ACA	ATT	CCC	AAT	CTA	TCC	336
	Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser	
				100					105					110			
_						~~~	m a a			0.00	07.0		~ T ~	2.00	0.05	202	204
5								GGA									384
	Glu	Tyr		Asn	Ser	Ата	Ser	Gly	Pro	Leu	GLu	GTĀ		rre	Arg	Arg	
			115					120					125				
	GAT	TCG	CCC	AAA	TTC	AAG	GAC	CTC	GTG	CCC	AAC	TAC	AAC	AGG	GAC	ATC	432
10	Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile	
		130					135					140					
	C III III	mm.c	CCT	CAC	CAC	C 7 7	CCC	7.00	CCA	CCC	CAT	ccc	መሞር	አጥር	A.C.C	AAC	480
								ACC									400
15		Pne	ΑτĠ	Asp	Glu	150	сту	Thr	GTĀ	Ala	155	GTA	ьеи	Met	ser	160	
13	145					1.00					100					100	
	CGC	TGC	AAG	GAG	AAG	СТА	AAC	GīĠ	CTG	GCC	TAC	TCG	GTG	ATG	AAC	GAA	528
	Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn	Glu	
					165					170					175		
20																	
	TGG	CCC	GGC	ATC	CGG	CTG	CTG	GTC	ACC	GAG	AGC	TGG	GAC	GAG	GAC	TAC	576
	Trp	Pro	Gly	Ile	Arg	Leu	Leu	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp	Tyr	
				180					185					190			
25	CAT	CAC	GGC	CAG	GAG	TCG	CTC	CAC	TAC	GAG	GGC	CGA	GCG	GTG	ACC	ATT	624
	His	His	_	Gln	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg		Val	Thr	Ile	
			195					200					205				
	GCC	ACC	TCC	GAT	CGC	GAC	CAG	TCC	AAA	TAC	GGC	ATG	CTC	GCT	CGC	CTG	672
30	Ala	Thr	Ser	Asp	Arq	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu	
		210		-	,	•	215		-	•	-	220			_		
	GCC	GTC	GAG	GCT	GGA	TTC	GAT	TGG	GTC	TCC	TAC	GTC	AGC	AGG	CGC	CAC	720
	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Ser	Tyr	Val	Ser	Arg	Arg	His	
35	225					230					235					240	
	7.00	mr.c	mc c	mcc.	C.T.C	D 72 C	m $\wedge$ n	CT T	шСС	mcc.	TA LET C	7 C FF	mcc.	CT C	C TH C	CAC	7.00
								GAT									768
	тте	Tyr	Cys	ser		ьуs	ser	Asp	ser		тте	ser	ser	HIS		піѕ	
					245					250					255		

	GGC	ፐርር	ጥጥር	ACG	CCG	GAG	AGC	ACA	GCG	СТС	СТС	GAG	АСТ	GGA	GTC	CGG	816
												Glu					010
	1	-1-		260					265					270		9	
5																	
	AAG	CCG	CTC	GGC	GAG	CTC	TCT	ATC	GGA	GAT	CGT	GTT	TTG	AGC	ATG	ACC	864
	Lys	Pro	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Asp	Arg	Val	Leu	Ser	Met	Thr	
			275					280					285				
10	GCC	AAC	GGA	CAG	GCC	GTC	TAC	AGC	GAA	GTG	ATC	CTC	TTC	ATG	GAC	CGC	912
	Ala	Asn	Gly	Gln	Ala	Val	_	Ser	Glu	Val	Ile	Leu	Phe	Met	Asp	Arg	
		290					295					300					
		~~~		~~~		~~~	776		C.T.C	070	G.T.G	G7.G	7.00	C 7 C	a a m	CCA	0.60
15												CAC His					960
15	305	ьеа	GIU	GIII	Mec	310	ASII	FIIE	vai	GIII	315	птэ	1111	АЗР	СТУ	320	
	303					310					313					320	
	GCA	GTG	CTC	ACG	GTG	ACG	CCG	GCT	CAC	CTG	GTT	AGC	GTT	TGG	CAG	CCG	1008.
	Ala	Val	Leu	Thr	Val	Thr	Pro	Ala	His	Leu	Val.	Ser	Val	Trp	Gln	Pro	
20					325					330					3.35		
	GAG	AGC	CAG	AAG	CTC	ACG	TTT	GTG	TTT	. GCG	CAT	·CGC	ATC	GAG	GAG	AAG	1056
	Glu	Ser	Gln	Lys	Leu	Thr	Phe	Val	Phe	Ala	His	Arg	Ile	Glu	Glu	Lys.	
				340					345					350			
25																	
												GAG					1104
	ASII	GIII	355	ьеи	vai	Arg	ASP	360	GIU	1111	GIY	Glu	365	Arg	PIO	GIH	
			333					300					303				
30	CGA	GTG	GTC	AAG	TTG	GGC	AGT	GTG	CGC	AGT	AAG	GGC	GTG	GTC	GCG	CCG	1152
	Arg	Val	Val	Lys	Leu	Gly	Ser	Val	Arg	Ser	Lys	Gly	Val	Val	Ala	Pro	
		370					375					380					
,	CTG	ACC	CGC	GAG	GGC	ACC	ATT	GTG	GTC	AAC	TCG	GTG	GCC	GCC	AGT	TGC	1200
35	Leu	Thr	Arg	Glu	Gly	Thr	Ile	Val	Val	Asn	Ser	Val	Ala	Ala	Ser	Cys	
	385					390					395					400	
																,	
												TGG					1248
	Tyr	Ala	Val	Ile	Asn	Ser	Gln	Ser			His	Trp	GLy	Leu	Ala	Pro	
									4	54/61							

					405					410					415		
	ATG	CGC	CTG	CTG	TCC	ACG	CTG	GAG	GCG	TGG	CTG	CCC	GCC	AAG	GAG	CAG	1296
	Met	Arg	Leu	Leu	Ser	Thr	Leu	Glu	Ala	Trp	Leu	Pro	Ala	Lys	Glu	Gln	
5				420					425					430			
	TTG	CAC	AGT	TCG	CCG	AAG	GTG	GTG	AGC	TCG	GCG	CAG	CAG	CAG	AAT	GGC	1344
	Leu	His	Ser	Ser	Pro	Lys	Val	Val	Ser	Ser	Ala	Gln	Gln	Gln	Asn	Gly	
			435					440					445				
10																	
	ATC	CAT	TGG	TAT	GCC	AAT	GCG	CTC	TAC	AAG	GTC	AAG	GAC	TAC	GTG	CTG	1392
	Ile	His	Trp	Tyr	Ala	Asn	Ala	Leu	Tyr	Lys	Val	Lys	Asp	Tyr	Val	Leu	
		450					455					460					
15	CCG	CAG	AGC	TGG	CGC	CAC	GAT	TGA									141.6
	Pro	Gln	Ser	Trp	Arg	His	Asp										
	465					470											
20	(2)	INFO	ORMA!	NOLT	FOR	SEQ	ID 1	io:20):							• ,	
•		-	(1) 3	SEQUE													
				, ,			47.			ac J. as	5						•
25							amino										
25	•			(D)	101	POLOC	3Y: 3	Linea	ı L								
		(;	i i) N	MOLEC	ים דווי	TVDI	r. ni	cotei	n								
		(-1	L1) I	1OLLEC	20115	IIFI	5. Pi	.0061	. 11								
		(5	zi) S	SEQUE	ENCE	DESC	ים ד פי	· TON ·	SEC	מד כ	NO: 2	20:					
30		(2	11)	JEQUE	31100		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		220	2 10							
50	Met	Asn	Asn	His	Ser	Ser	Val	Pro	Trp	Ala	Ser	Ala	Ala	Ser	Val	Thr	
	1	1101			5					10					15		
	_																
	Cvs	Leu	Ser	Leu	Glv	Cvs	Gln	Met	Pro	Gln	Phe	Gln	Phe	Gln	Phe	Gln	
35	-			20	-	-			25					30			
	Leu	Gln	Ile	Arg	Ser	Glu	Leu	His	Leu	Arg	Lys	Pro	Ala	Arg	Arg	Thr	

		Gln	Thr 50	Met	Arg	His	Ile	Ala 55	His	Thr	Gln	Arg	Cys 60	Leu	Ser	Arg	Leu
ø	5	Thr 65	Ser	Leu	Val	Ala	Leu 70	Leu	Leu	Ile	Val	Leu 75	Pro	Met	Val	Phe	Ser 80
		Pro	Ala	His	Ser	Cys 85	Gly	Pro	Gly	Arg	Gly 90	Leu	Gly	Arg	His	Arg 95	Ala
	10	Arg	Asn	Leu	Tyr 100	Pro	Leu	Val	Leu · ·	Lys 105	Gln	Thr	Ile	Pro	Asn 110	Leu	Ser
	15	Glu	Tyr	Thr 115	Asn	Ser	Ala	Ser	Gly 120	Pro	Leu	Glu	Gly	Val 125	Ile	Arg	Arg
4 4 6 6 6 6 6 6		Asp	Ser 130	Pro	Lys	Phe	Lys	Asp 135	Leu	Val	Pro	Asn	Tyr 140	Asn	Arg	Asp	Ile
	20	Leu 145	Phe	Arg	Asp	Glu	Glu 150	Gly	Thr	Gly	Ala	Asp 155	Gly	Leu	Met	Ser	Lys
		Arg	Cys	Lys	Glu	Lys 165	Leu	Asn	Val	Leu	Ala 170	Tyr	Ser	Val	Met	Asn 175	Glu
	25 .	Trp	Pro	Gly	Ile 180	Arg	Leu	Leu	Val	Thr 185	Glu	Ser	Trp	Asp	Glu 190	Asp	Tyr
	30	His	His	Gly 195	Gln	Glu	Ser	Leu	His 200		Glu	Gly	Arg	Ala 205	Val	Thr	Ile
		Ala	Thr 210	Ser	Asp	Arg	Asp	Gln 215	Ser	Lys	Tyr	Gly	Met 220	Leu	Ala	Arg	Leu
	35	Ala 225	Val	Glu	Ala	Gly	Phe 230	Asp	Trp	Val	Ser	Tyr 235	Val	Ser	Arg	Arg	His 240
		Ile	Tyr	Cys	Ser	Val 245	Lys	Ser	Asp	Ser	Ser 250	Ile	Ser	Ser	His	Val 255	His

	Gly	Cys	Phe	Thr 260	Pro	Glu	Ser	Thr	Ala 265	Leu	Leu	Glu	Ser	Gly 270	Val	Arg
5	Lys	Pro	Leu 275	Gly	Glu	Leu	Ser	Ile 280	Gly	Asp	Arg	Val	Leu 285	Ser	Met	Thr
	Ala	Asn 290	Gly	Gln	Ala	Val	Tyr 295	Ser	Glu	Val	Ile	Leu 300	Phe	Met	Asp	Arg
10	Asn 305	Leu	Glu	Gln	Met	Gln 310	Asn	Phe	Val	Gln	Leu 315	His	Thr	Asp	Gly	Gly 320
15	Ala	Val	Leu	Thr	Val 325	Thr	Pro	Ala	His	.Leu 330	Val	Ser	Val	Trp	Gln 335	Pro
	Glu	Ser	Gln	Lys 340	Leu	Thr	Phe	Val	Phe 345	Ala	His	Arg	Ile	Glu 350	Glu	Lys
20	Asn	Gl.n	Val 355	Leu	Val.	Arg	Asp	Val 360	Glu	Thr	Gly	Glu	Leu 365	Arg	Pro	Gln
	Arg	Val 370	Val	Lys	Leu	Gly	Ser 375	Val	Arg	Ser	Lys	Gly 380	Val	Val	Ala	Pro
25	Leu 385	Thr	Arg	Glu	Gly	Thr 390	Ile	Val	Val	Asn	Ser 395	Val	Ala	Ala	Ser	Cys 400
30	Tyr	Ala	Val	Ile	Asn 405	Ser	Gln	Ser	Leu	Ala 410	His	Trp	Gly	Leu	Ala 415	Pro
30	Met	Arg	Leu	Leu 420	Ser	Thr	Leu •	Glu	Ala 425	Trp	Leu	Pro	Ala	Lys 430	Glu	Gln
35	Leu	His	Ser 435	Ser	Pro	Lys	Val	Val 440	Ser	Ser	Ala	Gln	Gln 445	Gln	Asn	Gly
	Ile	His 450	Trp	Tyr	Ala	Asn	Ala 455	Leu	Tyr	Lys	Val	Lys 460	Asp	Tyr	Val	Leu

Pro Gln Ser Trp Arg His Asp 465 470

(2) INFORMATION FOR SEQ ID NO:21:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

15

20

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Leu

1 5 10 15

Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
20 25 30

Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu
35 40 45

Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys 50 55 60

Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
65 70 75 80

Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
85 90 95

Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa 100 105 110

35

Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser 115 120 125 Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu 5 130 135 140 Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys 145 150 155 160 10 Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe 165 170 175 Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Kaa Gly Gly Xaa Lys Xaa Val 180 185 190 15 Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Kaa Gly 195 200 205 Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg 210 215 220 20 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

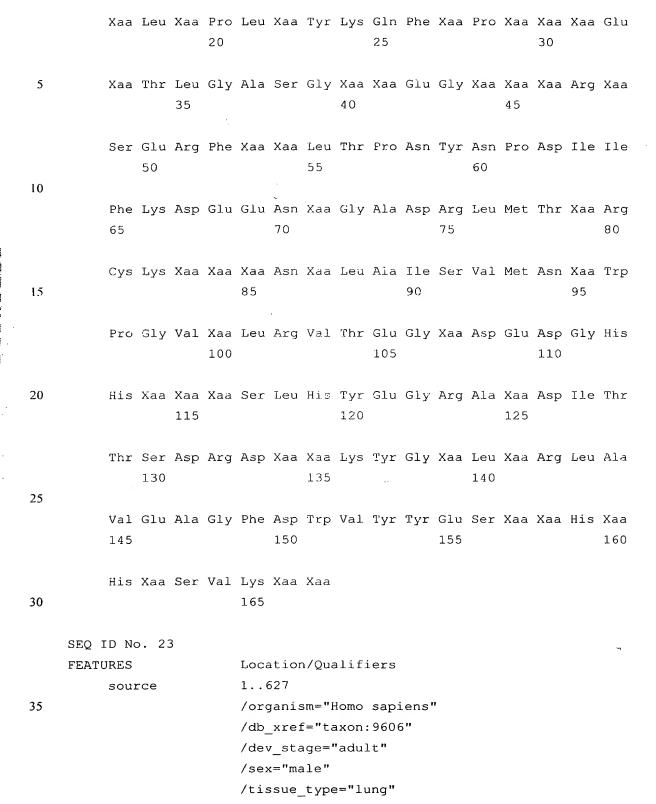
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys 1 5 10 15



60/61

```
1..627
          CDS
                          /standard name="fibroblast growth factor-10"
                          /codon start=1
                          /product="FGF-10"
 5
                          /protein id="BAA22331.1"
                          /db xref="PID:d1023194"
                          /db xref="PID:g2440221"
                          /db xref="GI:2440221"
             1 atgtggaaat ggatactgac acattgtgcc tcagcctttc cccacctgcc cggctgctgc
10
            61 tgctqctqct ttttgttqct qttcttgqtq tcttccqtcc ctgtcacctq ccaaqccctt
           121 ggtcaggaca tggtgtcacc agaggccacc aactettett cetecteett etecteet
           181 tocagegegg gaaggeatgt geggagetae aateacette aaggagatgt eegetggaga
           241 aagetattet ettteaceaa gtaetttete aagattgaga agaaegggaa ggteageggg
           301 accaagaagg agaactgccc gtacagcatc ctggagataa catcagtaga aatcggagtt
15
           361 gttgccgtca aagccattaa cagcaactat tacttagcca tgaacaagaa ggggaaactc
           421 tatggctcaa aagaatttaa caatgactgt aagctgaagg agaggataga ggaaaatgga
           481 tacaatacet atgeateatt taactggeag cataatggga ggeaaatgta tgtggeattg
           541 aatygaaaag gageteeaag gagaggacag aaaseaegaa ggaaaaaece etetgeteae
           601 tttcttccaa tggtggtaca ctcatag
20
    SEQ ID No. 24
     FEATURES
                          Location/Qualifiers
                          1..208
          source
                          /organism="Homo sapiens"
25
                          /db xref="taxon:9606"
                          /dev stage="adult"
                          /sex="male"
                          /tissue type="lung"
          Protein
                          1..208
30
                          /product="FGF-10"
                          1..208
         CDS
                          /standard name="fibroblast growth factor-10"
                          /coded by="GenBank Accesstion AB002097.1:1..627"
    ORIGIN
35
            1 mwkwilthca safphlpgcc cccflllflv ssvpvtcqal gqdmvspeat nsssssfssp
           61 ssagrhvrsy nhlqgdvrwr klfsftkyfl kiekngkvsg tkkencpysi leitsveigv
          121 vavkainsny ylamnkkgkl ygskefnndc klkerieeng yntyasfnwq hngrqmyval
          181 ngkgaprrgq ktrrkntsah flpmvvhs
```